

SEQUENCE LISTING

<110> Sheppard, Paul O.
Presnell, Scott R.

<120> MAMMALIAN SECRETED PROTEINS

<130> 00-41

<150> US 60/215,446

<151> 2000-06-30

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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ctg ctg gtt ttc tcc ctg cct gct ggc cta cat aca gcc ctc aca gca	96
Leu Leu Val Phe Ser Leu Pro Ala Gly Leu His Thr Ala Leu Thr Ala	
20 25 30	
gcc aga gga ctc ccc aaa ctg ccc aag cac agc cac atc gcc aaa gac	144
Ala Arg Gly Leu Pro Lys Leu Pro Lys His Ser His Ile Ala Lys Asp	
35 40 45	
acc cat tca tcc ttc cca tct cag ctc cag ggg ctg ctt tcc aaa gca	192
Thr His Ser Ser Phe Pro Ser Gln Leu Gln Gly Leu Leu Ser Lys Ala	
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"FastSeq" Seq. Editor

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			20					25					30		
Ala	Arg	Gly	Leu	Pro	Lys	Leu	Pro	Lys	His	Ser	His	Ile	Ala	Lys	Asp
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Thr	His	Ser	Ser	Phe	Pro	Ser	Gln	Leu	Gln	Gly	Leu	Leu	Ser	Lys	Ala
	50					55					60				
Thr	Pro	His	Arg	His	Pro	Cys	Asp	Ile	Ala	Gln	Phe	Lys	Thr	Val	Arg
65					70					75					80
Ile	Gln	Glu	Ser	Gln	Gln	Gln	Val	Val	Thr	Lys	Arg	Lys	Phe	Gln	His
				85					90					95	

Phe Thr Ala Ile His Arg Gln Gly Ser Tyr Val Tyr Gln Asp Asn Arg
 100 105 110
 Arg Thr Thr Glu His Arg Pro Ser Ser Ala Val Leu Leu Leu Pro Phe
 115 120 125
 Ala Leu Phe Pro Gln Lys His Val Ile Phe Val Arg Pro Leu Ser Val
 130 135 140
 Val Leu Leu Phe Ala Leu
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<220>
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1 5 10 15	
gtc cct ccc ctc atc ttc tta ctt tta ccc agc aga tct acc cgt ggg	96
Val Pro Pro Leu Ile Phe Leu Leu Leu Pro Ser Arg Ser Thr Arg Gly	
20 25 30	
cag ccc ttt tcc caa gta cca ggg gag aaa atg gat tca gaa aag gat	144
Gln Pro Phe Ser Gln Val Pro Gly Glu Lys Met Asp Ser Glu Lys Asp	
35 40 45	
ttg tgg gga gag gag ctt cca cac tta ata ctg aaa gag gct ttt cat	192
Leu Trp Gly Glu Glu Leu Pro His Leu Ile Leu Lys Glu Ala Phe His	
50 55 60	
ctg ttt ttc aag cca aca gca gcc cca ttc cca gat tca ctc aag gtc	240
Leu Phe Phe Lys Pro Thr Ala Ala Pro Phe Pro Asp Ser Leu Lys Val	
65 70 75 80	
tcc ctt aca tgt ccc tgg aaa gaa gga ggg tca cat aca aga tgc cag	288
Ser Leu Thr Cys Pro Trp Lys Glu Gly Gly Ser His Thr Arg Cys Gln	
85 90 95	

303

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      20             25             30
Gln Pro Phe Ser Gln Val Pro Gly Glu Lys Met Asp Ser Glu Lys Asp
      35             40             45
Leu Trp Gly Glu Glu Leu Pro His Leu Ile Leu Lys Glu Ala Phe His
      50             55             60
Leu Phe Phe Lys Pro Thr Ala Ala Pro Phe Pro Asp Ser Leu Lys Val
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Ser Leu Thr Cys Pro Trp Lys Glu Gly Gly Ser His Thr Arg Cys Gln
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Ser Gly Ser Arg
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1				5					10					15		
ctg	ttt	aaa	tgg	aaa	aga	aga	gta	gta	agt	ggt	cat	ctt	ctc	agc	gtc	96
Leu	Phe	Lys	Trp	Lys	Arg	Arg	Val	Val	Ser	Gly	His	Leu	Leu	Ser	Val	
			20					25					30			

tgg tgc tgg tcc cgc cca cac act gtg gca gag cag acc cac ctg ttg 144
 Trp Cys Trp Ser Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu
 35 40 45

tca ctg gga aat gag ggg ctg cag gta ctg ccc tta gac aat gga ggt 192
 Ser Leu Gly Asn Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Gly
 50 55 60

ggc caa gga cgt ttg ggg aca gat tac agg aaa gct caa caa ttc cct 240
 Gly Gln Gly Arg Leu Gly Thr Asp Tyr Arg Lys Ala Gln Gln Phe Pro
 65 70 75 80

tca tgc ttt ggt gtt gag cac tgg cct cct ttt taa 276
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<211> 91

<212> PRT

<213> Homo sapiens

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 20 25 30
 Trp Cys Trp Ser Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu
 35 40 45
 Ser Leu Gly Asn Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Gly
 50 55 60
 Gly Gln Gly Arg Leu Gly Thr Asp Tyr Arg Lys Ala Gln Gln Phe Pro
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 Ser Cys Phe Gly Val Glu His Trp Pro Pro Phe
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<212> DNA

<213> Homo sapiens

<220>

"GCG" sequence

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1				5					10					15		
tgg	gcc	tcc	gtg	agc	gcc	cag	acc	gat	gcc	acc	ccg	gcg	gtg	acg	aca	96
Trp	Ala	Ser	Val	Ser	Ala	Gln	Thr	Asp	Ala	Thr	Pro	Ala	Val	Thr	Thr	
			20					25					30			
gag	ggc	ctc	aac	tcc	acc	gag	gca	gcc	ctg	gcc	acc	ttc	gga	act	ttc	144
Glu	Gly	Leu	Asn	Ser	Thr	Glu	Ala	Ala	Leu	Ala	Thr	Phe	Gly	Thr	Phe	
		35					40					45				
ccg	tcg	acc	agg	ccc	ccc	ggg	act	ccc	agg	gct	cca	ggg	ccc	tcc	tcc	192
Pro	Ser	Thr	Arg	Pro	Pro	Gly	Thr	Pro	Arg	Ala	Pro	Gly	Pro	Ser	Ser	
	50					55					60					
ggc	ccc	agg	cct	acc	cca	gtc	acg	gac	gtt	gct	gtt	ctc	tgt	gtc	tgt	240
Gly	Pro	Arg	Pro	Thr	Pro	Val	Thr	Asp	Val	Ala	Val	Leu	Cys	Val	Cys	
65					70				75						80	
gac	tta	tcc	cca	gca	cag	tgt	gac	atc	aac	tgc	tgc	tgt	gat	ccc	gac	288
Asp	Leu	Ser	Pro	Ala	Gln	Cys	Asp	Ile	Asn	Cys	Cys	Cys	Asp	Pro	Asp	
				85					90					95		
tgc	agc	tcc	gtg	gat	ttc	agt	gtc	ttt	tct	gcc	tgc	tca	gtt	cca	gtt	336
Cys	Ser	Ser	Val	Asp	Phe	Ser	Val	Phe	Ser	Ala	Cys	Ser	Val	Pro	Val	
			100					105					110			
gtc	aca	ctt	act	gga	gct	ctc	ccg	tgt	cag	ctc	gta	gca	cag	aag	gtg	384
Val	Thr	Leu	Thr	Gly	Ala	Leu	Pro	Cys	Gln	Leu	Val	Ala	Gln	Lys	Val	
		115					120					125				
aag	agc	ctg	ctg	tgg	ggc	cag	ggc	ttc	cca	gat	tac	gtg	gcc	cct	ttt	432
Lys	Ser	Leu	Leu	Trp	Gly	Gln	Gly	Phe	Pro	Asp	Tyr	Val	Ala	Pro	Phe	
	130					135					140					
gga	aat	tcc	cag	gcc	cag	gac	atg	ctg	gac	tgg	tgc	cca	tcc	act	tca	480
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<213> Homo sapiens

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			20					25					30			
Glu	Gly	Leu	Asn	Ser	Thr	Glu	Ala	Ala	Leu	Ala	Thr	Phe	Gly	Thr	Phe	
		35				40						45				
Pro	Ser	Thr	Arg	Pro	Pro	Gly	Thr	Pro	Arg	Ala	Pro	Gly	Pro	Ser	Ser	
	50					55					60					
Gly	Pro	Arg	Pro	Thr	Pro	Val	Thr	Asp	Val	Ala	Val	Leu	Cys	Val	Cys	
65					70					75					80	
Asp	Leu	Ser	Pro	Ala	Gln	Cys	Asp	Ile	Asn	Cys	Cys	Cys	Asp	Pro	Asp	
				85					90					95		
Cys	Ser	Ser	Val	Asp	Phe	Ser	Val	Phe	Ser	Ala	Cys	Ser	Val	Pro	Val	
			100					105					110			
Val	Thr	Leu	Thr	Gly	Ala	Leu	Pro	Cys	Gln	Leu	Val	Ala	Gln	Lys	Val	
		115					120					125				
Lys	Ser	Leu	Leu	Trp	Gly	Gln	Gly	Phe	Pro	Asp	Tyr	Val	Ala	Pro	Phe	
	130					135					140					
Gly	Asn	Ser	Gln	Ala	Gln	Asp	Met	Leu	Asp	Trp	Cys	Pro	Ser	Thr	Ser	
145					150					155					160	
Ser	Pro	Ser	His	Ser	Thr	Gly	Arg	Trp	Cys	Asp	Glu	Gly	Ser	Arg	Gly	
				165					170					175		
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Asn Leu Gly Tyr 180 185 190
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<220>
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<222> (1)...(1200)

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1 5 10 15

ccg ctg tgg tcc tcc tca ctg cct ggg ctg gac act gct gaa agt aaa 96
Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
20 25 30

gcc acc att gca gac ctg atc ctg tct gcg ctg gag aga gcc acc gtc 144
Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
35 40 45

ttc cta gaa cag agg ctg cct gaa atc aac ctg gat ggc atg gtg ggg 192
Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
50 55 60

gtc cga gtg ctg gaa gcc ctg cgt gaa tgc tct cac tcg gat gtt ctc 240
Val Arg Val Leu Glu Ala Leu Arg Glu Cys Ser His Ser Asp Val Leu
65 70 75 80

act cat gtc tcc cca att tct ggc cac ctc tgg atc ttc acc att gtc 288
Thr His Val Ser Pro Ile Ser Gly His Leu Trp Ile Phe Thr Ile Val
85 90 95

tcc cac ctc aac aaa gcc act gct agc cca cag gag cag cta aaa agt 336
Ser His Leu Asn Lys Ala Thr Ala Ser Pro Gln Glu Gln Leu Lys Ser
100 105 110

gtc cgg gag aag tgg gcc cag gag ccc ctg ctg cag ccg ctg agc ctg 384

CCDS: F46860

Val Arg Glu Lys Trp Ala Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu	
115 120 125	
cgc gtg ggg atg ctg ggg gag aag ctg gag gct gcc atc cag aga tcc	432
Arg Val Gly Met Leu Gly Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser	
130 135 140	
ctc cac tac ctc aag ctg agt gat ccc aag tac cta aga gag ttc cag	480
Leu His Tyr Leu Lys Leu Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln	
145 150 155 160	
ctg acc ctc cag ccc ggg ttt tgg aag ctc cca cat gcc tgg atc cac	528
Leu Thr Leu Gln Pro Gly Phe Trp Lys Leu Pro His Ala Trp Ile His	
165 170 175	
act gat gcc tcc ttg gtg tac ccc acg ttc ggg ccc cag gac tca ttc	576
Thr Asp Ala Ser Leu Val Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe	
180 185 190	
tca gag gag aga agt gac gtg tgc ctg gtg cag ctg ctg gga acc ggg	624
Ser Glu Glu Arg Ser Asp Val Cys Leu Val Gln Leu Leu Gly Thr Gly	
195 200 205	
acg gac agc agc gag ccc tgc ggc ctc tca gac ctc tgc agg agc ctc	672
Thr Asp Ser Ser Glu Pro Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu	
210 215 220	
atg acc aag ccc ggc tgc tca ggc tac tgc ctg tcc cac caa ctg ctc	720
Met Thr Lys Pro Gly Cys Ser Gly Tyr Cys Leu Ser His Gln Leu Leu	
225 230 235 240	
ttc ttc ctc tgg gcc aga atg agg ggg tgc aca cag gga cca ctc caa	768
Phe Phe Leu Trp Ala Arg Met Arg Gly Cys Thr Gln Gly Pro Leu Gln	
245 250 255	
cag agc cag gac tat atc aac ctc ttc tgc gcc aac atg atg gac ttg	816
Gln Ser Gln Asp Tyr Ile Asn Leu Phe Cys Ala Asn Met Met Asp Leu	
260 265 270	
aac cgc aga gct gag gcc atc gga tac gcc tac cct acc cgg gac atc	864
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275 280 285	

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			20					25					30		
Ala	Thr	Ile	Ala	Asp	Leu	Ile	Leu	Ser	Ala	Leu	Glu	Arg	Ala	Thr	Val
		35					40					45			
Phe	Leu	Glu	Gln	Arg	Leu	Pro	Glu	Ile	Asn	Leu	Asp	Gly	Met	Val	Gly
	50					55					60				

Val 65	Arg	Val	Leu	Glu	Ala	Leu	Arg	Glu	Cys	Ser	His	Ser	Asp	Val	Leu
Thr	His	Val	Ser	Pro	Ile	Ser	Gly	His	Leu	Trp	Ile	Phe	Thr	Ile	Val
Ser	His	Leu	Asn	Lys	Ala	Thr	Ala	Ser	Pro	Gln	Glu	Gln	Leu	Lys	Ser
Val	Arg	Glu	Lys	Trp	Ala	Gln	Glu	Pro	Leu	Leu	Gln	Pro	Leu	Ser	Leu
Arg	Val	Gly	Met	Leu	Gly	Glu	Lys	Leu	Glu	Ala	Ala	Ile	Gln	Arg	Ser
Leu	His	Tyr	Leu	Lys	Leu	Ser	Asp	Pro	Lys	Tyr	Leu	Arg	Glu	Phe	Gln
Leu	Thr	Leu	Gln	Pro	Gly	Phe	Trp	Lys	Leu	Pro	His	Ala	Trp	Ile	His
Thr	Asp	Ala	Ser	Leu	Val	Tyr	Pro	Thr	Phe	Gly	Pro	Gln	Asp	Ser	Phe
Ser	Glu	Glu	Arg	Ser	Asp	Val	Cys	Leu	Val	Gln	Leu	Leu	Gly	Thr	Gly
Thr	Asp	Ser	Ser	Glu	Pro	Cys	Gly	Leu	Ser	Asp	Leu	Cys	Arg	Ser	Leu
Met	Thr	Lys	Pro	Gly	Cys	Ser	Gly	Tyr	Cys	Leu	Ser	His	Gln	Leu	Leu
Phe	Phe	Leu	Trp	Ala	Arg	Met	Arg	Gly	Cys	Thr	Gln	Gly	Pro	Leu	Gln
Gln	Ser	Gln	Asp	Tyr	Ile	Asn	Leu	Phe	Cys	Ala	Asn	Met	Met	Asp	Leu
Asn	Arg	Arg	Ala	Glu	Ala	Ile	Gly	Tyr	Ala	Tyr	Pro	Thr	Arg	Asp	Ile
Phe	Met	Glu	Asn	Ile	Met	Phe	Cys	Gly	Met	Gly	Gly	Phe	Ser	Asp	Phe
Tyr	Lys	Leu	Arg	Trp	Leu	Glu	Ala	Ile	Leu	Ser	Trp	Gln	Lys	Gln	Gln
Glu	Gly	Cys	Phe	Gly	Glu	Pro	Asp	Ala	Glu	Asp	Glu	Glu	Leu	Ser	Lys
Ala	Ile	Gln	Tyr	Gln	Gln	His	Phe	Ser	Arg	Arg	Val	Lys	Arg	Arg	Glu
Lys	Gln	Phe	Pro	Asp	Gly	Cys	Ser	Ser	His	Asn	Thr	Ala	Thr	Ala	Val
Ala	Ala	Leu	Gly	Gly	Phe	Leu	Tyr	Ile	Leu	Ala	Glu	Tyr	Pro	Pro	Ala
Asn	Arg	Glu	Pro	His	Pro	Ser	Thr	Pro	Pro	Pro	Pro	Ser	Ser	Arg	

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<220>
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1 5 10 15	
gct gac agc ttg cag gtg att agt ggg aaa gct cag tgt gtg act gct	96
Ala Asp Ser Leu Gln Val Ile Ser Gly Lys Ala Gln Cys Val Thr Ala	
20 25 30	
gtg act ttg gct att ccc aca cag aga aat gtg gca cca agg tgc ttt	144
Val Thr Leu Ala Ile Pro Thr Gln Arg Asn Val Ala Pro Arg Cys Phe	
35 40 45	
ggg gag gat gca caa gtg gca gcc tcc tgc aag atg ctg aag gac ttt	192
Gly Glu Asp Ala Gln Val Ala Ala Ser Cys Lys Met Leu Lys Asp Phe	
50 55 60	
ttg ctg gtt gca ctg gcc ttc act ggt gtc act ctg ttg ctg ctc ctg	240
Leu Leu Val Ala Leu Ala Phe Thr Gly Val Thr Leu Leu Leu Leu Leu	
65 70 75 80	
tga	243
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1 5 10 15


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85 90 95

tct gcg ggg gac cag gat gtg tcc aat aag gca ccc atg tcc aac act 336
 Ser Ala Gly Asp Gln Asp Val Ser Asn Lys Ala Pro Met Ser Asn Thr
 100 105 110

gcc cag ggc agc aac atc ttt gag aga atg gag gtc gtg gca gtc ctg 384
 Ala Gln Gly Ser Asn Ile Phe Glu Arg Met Glu Val Val Ala Val Leu
 115 120 125

att gtg gac agc atc gcg ggc atc ctc tct gct gtt ttc ctg atc ctg 432
 Ile Val Asp Ser Ile Ala Gly Ile Leu Ser Ala Val Phe Leu Ile Leu
 130 135 140

ctt ctg gtg aac cat atg aag aag gat gaa ggc aga aac gac ctg agc 480
 Leu Leu Val Asn His Met Lys Lys Asp Glu Gly Arg Asn Asp Leu Ser
 145 150 155 160

agg aag ccc atc tac aaa aaa gcc cct agc aag gag tta tta cgc ttc 528
 Arg Lys Pro Ile Tyr Lys Lys Ala Pro Ser Lys Glu Leu Leu Arg Phe
 165 170 175

ttc tat gag cac tgg ttt gga ctt tag 555
 Phe Tyr Glu His Trp Phe Gly Leu *
 180

<210> 14

<211> 184

<212> PRT

<213> Homo sapiens

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Met Thr His Tyr Phe Arg Glu Thr Gln Glu Glu Gly Cys Ser Pro Ser
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 Leu Leu Phe Ala Gly Thr Pro Thr Pro Glu Ser Ile Gln Glu Thr
 35 40 45
 Glu Val Ile Asn Pro Gly Pro Pro Arg Gly Gln Thr Ser Pro Asp Pro
 50 55 60
 Tyr Trp Lys Thr Leu Asp Gly Arg Ala Trp Glu Pro Gly Pro Thr Glu
 65 70 75 80
 Thr Lys Glu Leu Glu Asp Asn Glu Val Ile Pro Arg Arg Ile Ser Leu
 85 90 95

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1			5			10			15							
tgg	ctg	gcc	tgg	gcc	ccg	gct	gcc	tct	gcc	tac	agt	gcc	atc	cac	gct	96
Trp	Leu	Ala	Trp	Ala	Pro	Ala	Ala	Ser	Ala	Tyr	Ser	Ala	Ile	His	Ala	
20			25			30										
agg	gaa	cag	ctg	tcc	cca	caa	gaa	cca	tgt	ggt	cca	tgt	ctg	ggc	agt	144
Arg	Glu	Gln	Leu	Ser	Pro	Gln	Glu	Pro	Cys	Gly	Pro	Cys	Leu	Gly	Ser	
35			40			45										
gac	cgc	ctc	act	tgc	agc	caa	ccc	cac	act	ctt	cag	tgg	tgc	cga	ggt	192
Asp	Arg	Leu	Thr	Cys	Ser	Gln	Pro	His	Thr	Leu	Gln	Trp	Cys	Arg	Gly	
50			55			60										
cct	gtg	gca	gac	tca	gcc	aat	ccc	agt	gtg	gac	ttg	act	cgg	tct	tgg	240
Pro	Val	Ala	Asp	Ser	Ala	Asn	Pro	Ser	Val	Asp	Leu	Thr	Arg	Ser	Trp	
65			70			75			80							

<400> 16															
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1				5					10					15	
Trp	Leu	Ala	Trp	Ala	Pro	Ala	Ala	Ser	Ala	Tyr	Ser	Ala	Ile	His	Ala
			20					25					30		
Arg	Glu	Gln	Leu	Ser	Pro	Gln	Glu	Pro	Cys	Gly	Pro	Cys	Leu	Gly	Ser
		35					40					45			
Asp	Arg	Leu	Thr	Cys	Ser	Gln	Pro	His	Thr	Leu	Gln	Trp	Cys	Arg	Gly
	50					55					60				

Pro Val Ala Asp Ser Ala Asn Pro Ser Val Asp Leu Thr Arg Ser Trp
 65 70 75 80
 Thr Pro Gly Ala Ser Glu Leu Ala Val Gly Pro Val Gly Leu Ser Leu
 85 90 95
 Ile Leu Asp Arg Ala Trp Thr Trp Gly Leu Trp Leu Gly Arg Gly Ala
 100 105 110
 Pro Val Trp Ala Asn Arg Thr Ala Asp Gly Leu Glu Asp Ser Val Thr
 115 120 125
 Glu Leu Ser Ala Ser Thr Arg Asp Ser Thr Trp Met Gln Arg Ser Pro
 130 135 140
 Leu Ala Ile Ser Gly Asp Thr Thr Pro Arg Ser Tyr Cys Ser Gln His
 145 150 155 160
 Cys Gln Ala Ala Thr Ser Gln Glu Asp Ile Ser Asn Lys Thr Lys Ser
 165 170 175
 Ile Phe Pro Ser Ser Trp Thr Thr Ala Met Trp Phe
 180 185

<210> 17
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(474)

<400> 17
 atg cga ttg tgg ttc acc gca gtc ttg acc tcc tgg gct caa gcc atc 48
 Met Arg Leu Trp Phe Thr Ala Val Leu Thr Ser Trp Ala Gln Ala Ile
 1 5 10 15
 ctc cct tct tgg cct ccc aat gtg gtg gta tta cag gcc ggg cct cca 96
 Leu Pro Ser Trp Pro Pro Asn Val Val Val Leu Gln Ala Gly Pro Pro
 20 25 30
 ctt tct cat gtc acc cac tct gct att act cca tgc tcc cat cct tcc 144
 Leu Ser His Val Thr His Ser Ala Ile Thr Pro Cys Ser His Pro Ser
 35 40 45
 tac gtc ctt act ttc acc cag gat gag aaa gtg ccc cac cgt gtc cag 192
 Tyr Val Leu Thr Phe Thr Gln Asp Glu Lys Val Pro His Arg Val Gln
 50 55 60

gcc aca tca cct tgt ccc atg acc tat gtc cct tcc ctc ccc aag gga 240
 Ala Thr Ser Pro Cys Pro Met Thr Tyr Val Pro Ser Leu Pro Lys Gly
 65 70 75 80

agc ttc agc cca tac ctt gcg cca ttt acc cgg ccc aag ggc tct ccc 288
 Ser Phe Ser Pro Tyr Leu Ala Pro Phe Thr Arg Pro Lys Gly Ser Pro
 85 90 95

tgc gca gga aag gcc gac ctc aca ctg cat gtg gat ggc gtg aca gtc 336
 Cys Ala Gly Lys Ala Asp Leu Thr Leu His Val Asp Gly Val Thr Val
 100 105 110

ctg aat gtg ggg aaa gag agc ttg tcc tcg cag cta cgt caa cag aag 384
 Leu Asn Val Gly Lys Glu Ser Leu Ser Ser Gln Leu Arg Gln Gln Lys
 115 120 125

cca gag act ggg gcc aag aag aaa gac cct gcg ggg ttg ggc tgg aaa 432
 Pro Glu Thr Gly Ala Lys Lys Lys Asp Pro Ala Gly Leu Gly Trp Lys
 130 135 140

gtc ctg gac gcc cag ctc ttc aca ccc act cag tgc atg tga 474
 Val Leu Asp Ala Gln Leu Phe Thr Pro Thr Gln Cys Met *
 145 150 155

<210> 18

<211> 157

<212> PRT

<213> Homo sapiens

<400> 18

Met Arg Leu Trp Phe Thr Ala Val Leu Thr Ser Trp Ala Gln Ala Ile
 1 5 10 15
 Leu Pro Ser Trp Pro Pro Asn Val Val Val Leu Gln Ala Gly Pro Pro
 20 25 30
 Leu Ser His Val Thr His Ser Ala Ile Thr Pro Cys Ser His Pro Ser
 35 40 45
 Tyr Val Leu Thr Phe Thr Gln Asp Glu Lys Val Pro His Arg Val Gln
 50 55 60
 Ala Thr Ser Pro Cys Pro Met Thr Tyr Val Pro Ser Leu Pro Lys Gly
 65 70 75 80
 Ser Phe Ser Pro Tyr Leu Ala Pro Phe Thr Arg Pro Lys Gly Ser Pro
 85 90 95

Cys Ala Gly Lys Ala Asp Leu Thr Leu His Val Asp Gly Val Thr Val
 100 105 110
 Leu Asn Val Gly Lys Glu Ser Leu Ser Ser Gln Leu Arg Gln Gln Lys
 115 120 125
 Pro Glu Thr Gly Ala Lys Lys Lys Asp Pro Ala Gly Leu Gly Trp Lys
 130 135 140
 Val Leu Asp Ala Gln Leu Phe Thr Pro Thr Gln Cys Met
 145 150 155

<210> 19
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(495)

<400> 19
 atg caa agg tgg aca ctg tgg gct gca gcc ttc ctg acc ctc cac tct 48
 Met Gln Arg Trp Thr Leu Trp Ala Ala Ala Phe Leu Thr Leu His Ser
 1 5 10 15

 gca cag gcc ttt cca caa aca gac atc agt atc agt cca gcc ctg cca 96
 Ala Gln Ala Phe Pro Gln Thr Asp Ile Ser Ile Ser Pro Ala Leu Pro
 20 25 30

 gag ctg ccc ctg cct tcc ctg tgc ccc ctg ttc tgg atg gag ttc aaa 144
 Glu Leu Pro Leu Pro Ser Leu Cys Pro Leu Phe Trp Met Glu Phe Lys
 35 40 45

 ggc cac tgc tat cga ttc ttc cct ctc aat aag acc tgg gct gag gcc 192
 Gly His Cys Tyr Arg Phe Phe Pro Leu Asn Lys Thr Trp Ala Glu Ala
 50 55 60

 gac ctc tac tgt tct gag ttc tct gtg ggc agg aag tcc gcc aag ctg 240
 Asp Leu Tyr Cys Ser Glu Phe Ser Val Gly Arg Lys Ser Ala Lys Leu
 65 70 75 80

 gcc tcc atc cac agc tgg gag gag aat gtc ttt gta tat gac ctc gtg 288
 Ala Ser Ile His Ser Trp Glu Glu Asn Val Phe Val Tyr Asp Leu Val
 85 90 95

"T00000" 220000

aac agc tgt gtt ccc ggc atc cca gct gac gtc tgg aca ggc ctt cat 336
 Asn Ser Cys Val Pro Gly Ile Pro Ala Asp Val Trp Thr Gly Leu His
 100 105 110

gat cac aga cag gaa ggg cag ttt gaa tgg act gat ggc tca tcc tat 384
 Asp His Arg Gln Glu Gly Gln Phe Glu Trp Thr Asp Gly Ser Ser Tyr
 115 120 125

gac tac agc tac tgg gat ggc agc cag cca gat gat ggc gtc cac gcg 432
 Asp Tyr Ser Tyr Trp Asp Gly Ser Gln Pro Asp Asp Gly Val His Ala
 130 135 140

gac cca gaa gaa gag gac tgc gtg cag ata tgg tac agg cct acc agt 480
 Asp Pro Glu Glu Glu Asp Cys Val Gln Ile Trp Tyr Arg Pro Thr Ser
 145 150 155 160

ggt ggg tac ccc tga 495
 Gly Gly Tyr Pro *

<210> 20
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Gln Arg Trp Thr Leu Trp Ala Ala Ala Phe Leu Thr Leu His Ser
 1 5 10 15
 Ala Gln Ala Phe Pro Gln Thr Asp Ile Ser Ile Ser Pro Ala Leu Pro
 20 25 30
 Glu Leu Pro Leu Pro Ser Leu Cys Pro Leu Phe Trp Met Glu Phe Lys
 35 40 45
 Gly His Cys Tyr Arg Phe Phe Pro Leu Asn Lys Thr Trp Ala Glu Ala
 50 55 60
 Asp Leu Tyr Cys Ser Glu Phe Ser Val Gly Arg Lys Ser Ala Lys Leu
 65 70 75 80
 Ala Ser Ile His Ser Trp Glu Glu Asn Val Phe Val Tyr Asp Leu Val
 85 90 95
 Asn Ser Cys Val Pro Gly Ile Pro Ala Asp Val Trp Thr Gly Leu His
 100 105 110
 Asp His Arg Gln Glu Gly Gln Phe Glu Trp Thr Asp Gly Ser Ser Tyr
 115 120 125


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<210> 21
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(531)
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<400> 21																
atg	ccc	agg	gtg	atg	gcc	tgg	agg	tac	tgg	gtc	cac	aca	gat	ggc	tgc	48
Met	Pro	Arg	Val	Met	Ala	Trp	Arg	Tyr	Trp	Val	His	Thr	Asp	Gly	Cys	
1			5			10			15							
tgc	agc	caa	ccc	tgc	cag	agt	ccc	caa	ggc	gcc	cta	gcc	atg	ctg	ccg	96
Cys	Ser	Gln	Pro	Cys	Gln	Ser	Pro	Gln	Gly	Ala	Leu	Ala	Met	Leu	Pro	
20			25			30										
ctt	gtg	cta	gcc	ttc	atc	agt	gaa	atc	tca	gcc	caa	cca	aac	cag	ttt	144
Leu	Val	Leu	Ala	Phe	Ile	Ser	Glu	Ile	Ser	Ala	Gln	Pro	Asn	Gln	Phe	
35			40			45										
cag	ggc	gcc	agc	tca	gtg	aca	ttc	att	tcc	aca	ctt	ttg	ttg	aac	ccg	192
Gln	Gly	Ala	Ser	Ser	Val	Thr	Phe	Ile	Ser	Thr	Leu	Leu	Leu	Asn	Pro	
50			55			60										
acc	ttc	act	aag	cac	tgg	ctc	tgc	acc	agg	agt	gtg	cgg	ggc	cct	ggc	240
Thr	Phe	Thr	Lys	His	Trp	Leu	Cys	Thr	Arg	Ser	Val	Arg	Gly	Pro	Gly	
65			70			75			80							
atg	cag	ggg	ccc	cag	gcc	agc	ccc	agc	cct	gct	ctg	gag	ctt	atg	atg	288
Met	Gln	Gly	Pro	Gln	Ala	Ser	Pro	Ser	Pro	Ala	Leu	Glu	Leu	Met	Met	
85			90			95										
gaa	ctt	aac	cag	aag	aag	cta	agg	aag	aga	aga	gag	gag	agg	aga	gag	336
Glu	Leu	Asn	Gln	Lys	Lys	Leu	Arg	Lys	Arg	Arg	Glu	Glu	Arg	Arg	Glu	

100	105	110	
aca gtg aag agg ctg gaa aag gag gaa gag aag tat gtt ctt tgg aat			384
Thr Val Lys Arg Leu Glu Lys Glu Glu Glu Lys Tyr Val Leu Trp Asn			
115	120	125	
caa agt gtt acc tgg att cct acc cag gat ttt cct att gtc tca gga			432
Gln Ser Val Thr Trp Ile Pro Thr Gln Asp Phe Pro Ile Val Ser Gly			
130	135	140	
cct aaa ggg aaa aga ccg gcc atg ggg cat aat ggg gac gat aca gga			480
Pro Lys Gly Lys Arg Pro Ala Met Gly His Asn Gly Asp Asp Thr Gly			
145	150	155	160
cct ccc tca tca gag ctg tca caa gtg aac ctc aat ttc ctg att ccc			528
Pro Pro Ser Ser Glu Leu Ser Gln Val Asn Leu Asn Phe Leu Ile Pro			
165	170	175	
taa			531
*			

<210> 22

<211> 176

<212> PRT

<213> Homo sapiens

<400> 22

Met Pro Arg Val Met Ala Trp Arg Tyr Trp Val His Thr Asp Gly Cys	
1 5 10 15	
Cys Ser Gln Pro Cys Gln Ser Pro Gln Gly Ala Leu Ala Met Leu Pro	
20 25 30	
Leu Val Leu Ala Phe Ile Ser Glu Ile Ser Ala Gln Pro Asn Gln Phe	
35 40 45	
Gln Gly Ala Ser Ser Val Thr Phe Ile Ser Thr Leu Leu Leu Asn Pro	
50 55 60	
Thr Phe Thr Lys His Trp Leu Cys Thr Arg Ser Val Arg Gly Pro Gly	
65 70 75 80	
Met Gln Gly Pro Gln Ala Ser Pro Ser Pro Ala Leu Glu Leu Met Met	
85 90 95	
Glu Leu Asn Gln Lys Lys Leu Arg Lys Arg Arg Glu Glu Arg Arg Glu	
100 105 110	

<210>	23	
<211>	282	
<212>	DNA	
<213>	Homo sapiens	
<220>		
<221>	CDS	
<222>	(1)...(282)	
<400>	23	
atg gcc cga tgt ccc ctc ctt ctg ttt ccc ctg ccg ctt gtc ccc atg		48
Met Ala Arg Cys Pro Leu Leu Leu Phe Pro Leu Pro Leu Val Pro Met		
1 5 10 15		
gcc ctg ggg gca tcc gca gga ggg agg cat gct ttt ggg tac cga cac		96
Ala Leu Gly Ala Ser Ala Gly Gly Arg His Ala Phe Gly Tyr Arg His		
20 25 30		
atg ttc ctc cag gag gag tgg tgg aaa gga gga atc ctt tgg cct cca		144
Met Phe Leu Gln Glu Glu Trp Trp Lys Gly Gly Ile Leu Trp Pro Pro		
35 40 45		
acc ctg gaa gaa ggg tcc atg tgg gag gaa aca gct cac agg tca tca		192
Thr Leu Glu Glu Gly Ser Met Trp Glu Glu Thr Ala His Arg Ser Ser		
50 55 60		
atg aga cat cgg aga gag ccg cta ggt gtt gtg gca gat gag gca gtg		240
Met Arg His Arg Arg Glu Pro Leu Gly Val Val Ala Asp Glu Ala Val		
65 70 75 80		
cct cca cgt gtg ctc atg ggc act ccc ggt cat gaa gag tga		282
Pro Pro Arg Val Leu Met Gly Thr Pro Gly His Glu Glu *		
85 90		

<210> 24
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 24

Met Ala Arg Cys Pro Leu Leu Leu Phe Pro Leu Pro Leu Val Pro Met
 1 5 10 15
 Ala Leu Gly Ala Ser Ala Gly Gly Arg His Ala Phe Gly Tyr Arg His
 20 25 30
 Met Phe Leu Gln Glu Glu Trp Trp Lys Gly Gly Ile Leu Trp Pro Pro
 35 40 45
 Thr Leu Glu Glu Gly Ser Met Trp Glu Glu Thr Ala His Arg Ser Ser
 50 55 60
 Met Arg His Arg Arg Glu Pro Leu Gly Val Val Ala Asp Glu Ala Val
 65 70 75 80
 Pro Pro Arg Val Leu Met Gly Thr Pro Gly His Glu Glu
 85 90

<210> 25
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(372)

<400> 25

atg ccc cct gac ccc aag gca ctg ctc tgc ctc aac ctc ccc cac ttc 48
 Met Pro Pro Asp Pro Lys Ala Leu Leu Cys Leu Asn Leu Pro His Phe
 1 5 10 15
 gcc ctg tgc cag ccc tgg gta ccc tcc ctg cag gcc gcg tcc ctc gcc 96
 Ala Leu Cys Gln Pro Trp Val Pro Ser Leu Gln Ala Ala Ser Leu Ala
 20 25 30
 acc tgg cct cct gtc ttc tgg aac tca ggc cct gcc ccc tgc tcc cag 144
 Thr Trp Pro Pro Val Phe Trp Asn Ser Gly Pro Ala Pro Cys Ser Gln
 35 40 45
 cct cca atg ccc acg tcc aac agg act ctg ctt ctc agc ccc acc tca 192


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<220>  
<221> CDS  
<222> (1)...(657)
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atg	gag	aca	gag	cct	tca	aag	gcc	aga	gcc	aat	gac	cca	gga	tca	gct	48
Met	Glu	Thr	Glu	Pro	Ser	Lys	Ala	Arg	Ala	Asn	Asp	Pro	Gly	Ser	Ala	
1				5					10					15		
gca	gag	ggg	ctc	agc	ctg	ttg	ctg	ctt	ccc	ttg	ctc	ctg	gtt	caa	gct	96
Ala	Glu	Gly	Leu	Ser	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Val	Gln	Ala	
			20					25					30			
ggt	gtc	tgg	gga	ttc	cca	agg	ccc	cca	ggg	agg	ccc	cag	ctg	agc	ctg	144
Gly	Val	Trp	Gly	Phe	Pro	Arg	Pro	Pro	Gly	Arg	Pro	Gln	Leu	Ser	Leu	
		35					40					45				
cag	gag	ctg	cgg	agg	gag	ttc	aca	gtc	agc	ctg	cat	ctc	gcc	agg	aag	192
Gln	Glu	Leu	Arg	Arg	Glu	Phe	Thr	Val	Ser	Leu	His	Leu	Ala	Arg	Lys	
	50					55					60					
ctg	ctc	tcc	gag	gtt	cgg	ggc	cag	gcc	cac	cgc	ttt	gac	ccg	gag	cgt	240
Leu	Leu	Ser	Glu	Val	Arg	Gly	Gln	Ala	His	Arg	Phe	Asp	Pro	Glu	Arg	
65					70					75					80	
ctc	tgc	ttc	atc	tcc	acc	acg	ctt	cag	ccc	ttc	cat	gcc	ctg	ctg	gga	288
Leu	Cys	Phe	Ile	Ser	Thr	Thr	Leu	Gln	Pro	Phe	His	Ala	Leu	Leu	Gly	
				85					90					95		
ggg	ctg	ggg	acc	cag	ggc	cgc	tgg	acc	aac	atg	gag	agg	atg	cag	ctg	336
Gly	Leu	Gly	Thr	Gln	Gly	Arg	Trp	Thr	Asn	Met	Glu	Arg	Met	Gln	Leu	
			100					105					110			
tgg	gcc	atg	agg	ctg	gac	ctc	cgc	gat	ctg	cag	cgg	cac	ctc	cgc	ttc	384
Trp	Ala	Met	Arg	Leu	Asp	Leu	Arg	Asp	Leu	Gln	Arg	His	Leu	Arg	Phe	
		115					120					125				
cag	gtg	ctg	gct	gca	gga	ttc	aac	ctc	ccg	gag	gag	gag	gag	gag	gaa	432

Met	Glu	Thr	Glu	Pro	Ser	Lys	Ala	Arg	Ala	Asn	Asp	Pro	Gly	Ser	Ala
1				5					10					15	
Ala	Glu	Gly	Leu	Ser	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Val	Gln	Ala
			20					25					30		
Gly	Val	Trp	Gly	Phe	Pro	Arg	Pro	Pro	Gly	Arg	Pro	Gln	Leu	Ser	Leu
		35					40					45			
Gln	Glu	Leu	Arg	Arg	Glu	Phe	Thr	Val	Ser	Leu	His	Leu	Ala	Arg	Lys
	50					55					60				
Leu	Leu	Ser	Glu	Val	Arg	Gly	Gln	Ala	His	Arg	Phe	Asp	Pro	Glu	Arg
65					70					75				80	
Leu	Cys	Phe	Ile	Ser	Thr	Thr	Leu	Gln	Pro	Phe	His	Ala	Leu	Leu	Gly
				85					90					95	
Gly	Leu	Gly	Thr	Gln	Gly	Arg	Trp	Thr	Asn	Met	Glu	Arg	Met	Gln	Leu

100 105 110
 Trp Ala Met Arg Leu Asp Leu Arg Asp Leu Gln Arg His Leu Arg Phe
 115 120 125
 Gln Val Leu Ala Ala Gly Phe Asn Leu Pro Glu Glu Glu Glu Glu
 130 135 140
 Glu Glu Glu Glu Glu Glu Glu Arg Lys Gly Leu Leu Pro Gly Ala Leu
 145 150 155 160
 Gly Ser Ala Leu Gln Gly Pro Ala Gln Val Ser Trp Pro Gln Leu Leu
 165 170 175
 Ser Thr Tyr Arg Leu Leu His Ser Leu Glu Leu Val Leu Ser Arg Ala
 180 185 190
 Val Arg Glu Leu Leu Leu Leu Ser Lys Ala Gly His Ser Val Trp Pro
 195 200 205
 Leu Gly Phe Pro Thr Leu Ser Pro Gln Pro
 210 215

<210> 29
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(533)

<400> 29

atg cac gtt cca gtg ata aag ctg tgc acg gca gcc atg gct atc cag	48
Met His Val Pro Val Ile Lys Leu Cys Thr Ala Ala Met Ala Ile Gln	
1 5 10 15	
ctg gcc cag ccc aac aga gat ctg tgg ttc ctc act tgc ctg cac ctt	96
Leu Ala Gln Pro Asn Arg Asp Leu Trp Phe Leu Thr Cys Leu His Leu	
20 25 30	
ctc tgc ctt ctc ctc tta cca tca cct cca ata tca gca ggt cct ggt	144
Leu Cys Leu Leu Leu Leu Pro Ser Pro Pro Ile Ser Ala Gly Pro Gly	
35 40 45	
cct tct ctg cct tct ccc ctc acc atc atg tcc aat atc agc agc tgc	192
Pro Ser Leu Pro Ser Pro Leu Thr Ile Met Ser Asn Ile Ser Ser Cys	
50 55 60	
cag agc ctg gcc cca cca tca tcc tct ccc agc tgg aca ggt gtt cct	240

Gln Ser Leu Ala Pro Pro Ser Ser Ser Pro Ser Trp Thr Gly Val Pro
65 70 75 80

gcc ttc caa gta ggg tcc cag cct cca ccc ttg gag gta gac cta cag 288
Ala Phe Gln Val Gly Ser Gln Pro Pro Pro Leu Glu Val Asp Leu Gln
85 90 95

gaa ctc ttc gga gag gac aag cgc ctt tta aag gtc gag cat cta tgc 336
Glu Leu Phe Gly Glu Asp Lys Arg Leu Leu Lys Val Glu His Leu Cys
100 105 110

tgc tgc ggc tac gta cct gtc acg agc atc caa cca att tgg ggc gcg 384
Cys Cys Gly Tyr Val Pro Val Thr Ser Ile Gln Pro Ile Trp Gly Ala
115 120 125

cat ctg ctg tgc tta aag ggc aag ttc aac act gtt aag ttt gtg ttg 432
His Leu Leu Cys Leu Lys Gly Lys Phe Asn Thr Val Lys Phe Val Leu
130 135 140

caa cga agc cag att gtg tgg gca caa tcc agt acc agg ggt ctg act 480
Gln Arg Ser Gln Ile Val Trp Ala Gln Ser Ser Thr Arg Gly Leu Thr
145 150 155 160

act aac agt cgc ata tta cct ccc tta tac ctc ccg tgt atg ctc cta 528
Thr Asn Ser Arg Ile Leu Pro Pro Leu Tyr Leu Pro Cys Met Leu Leu
165 170 175

gcc cg 533
Ala

<210> 30

<211> 177

<212> PRT

<213> Homo sapiens

<400> 30

Met His Val Pro Val Ile Lys Leu Cys Thr Ala Ala Met Ala Ile Gln
1 5 10 15
Leu Ala Gln Pro Asn Arg Asp Leu Trp Phe Leu Thr Cys Leu His Leu
20 25 30
Leu Cys Leu Leu Leu Leu Pro Ser Pro Pro Ile Ser Ala Gly Pro Gly

35 40 45
 Pro Ser Leu Pro Ser Pro Leu Thr Ile Met Ser Asn Ile Ser Ser Cys
 50 55 60
 Gln Ser Leu Ala Pro Pro Ser Ser Ser Pro Ser Trp Thr Gly Val Pro
 65 70 75 80
 Ala Phe Gln Val Gly Ser Gln Pro Pro Pro Leu Glu Val Asp Leu Gln
 85 90 95
 Glu Leu Phe Gly Glu Asp Lys Arg Leu Leu Lys Val Glu His Leu Cys
 100 105 110
 Cys Cys Gly Tyr Val Pro Val Thr Ser Ile Gln Pro Ile Trp Gly Ala
 115 120 125
 His Leu Leu Cys Leu Lys Gly Lys Phe Asn Thr Val Lys Phe Val Leu
 130 135 140
 Gln Arg Ser Gln Ile Val Trp Ala Gln Ser Ser Thr Arg Gly Leu Thr
 145 150 155 160
 Thr Asn Ser Arg Ile Leu Pro Pro Leu Tyr Leu Pro Cys Met Leu Leu
 165 170 175
 Ala

<210> 31
 <211> 525
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(525)

<400> 31
 atg gga gtc tca ctg gat cag gag cac agc aga cac cct gct gga tct 48
 Met Gly Val Ser Leu Asp Gln Glu His Ser Arg His Pro Ala Gly Ser
 1 5 10 15
 gga ggt atg gga gtc agc ggc agg tct gcg aca gtg gca aac agc agt 96
 Gly Gly Met Gly Val Ser Gly Arg Ser Ala Thr Val Ala Asn Ser Ser
 20 25 30
 ggt gga tgg atc ttt ggg gtg ttg ctt ttc tca ccg gaa acc tct gca 144
 Gly Gly Trp Ile Phe Gly Val Leu Leu Phe Ser Pro Glu Thr Ser Ala
 35 40 45
 gcc agt ggc atc ttt gcc caa gtt cat gtc ctg tgt cca gga aga atg 192

Ala Ser Gly Ile Phe Ala Gln Val His Val Leu Cys Pro Gly Arg Met
50 55 60

agg tat gca gac aag tgg agg agg gaa gga agt gca tgc cga ttg gtc 240
Arg Tyr Ala Asp Lys Trp Arg Arg Glu Gly Ser Ala Cys Arg Leu Val
65 70 75 80

cat agg cag cca tgg gct gct gga aaa ggc acc aca agt ccc cac tct 288
His Arg Gln Pro Trp Ala Ala Gly Lys Gly Thr Thr Ser Pro His Ser
85 90 95

gga cag tgg aat agc agc cca acc ccc agc ctt caa gac ctc cct ggc 336
Gly Gln Trp Asn Ser Ser Pro Thr Pro Ser Leu Gln Asp Leu Pro Gly
100 105 110

ctg aag aac aga aat ttg gct gct atg aaa ctt gac aag ccg atc ccc 384
Leu Lys Asn Arg Asn Leu Ala Ala Met Lys Leu Asp Lys Pro Ile Pro
115 120 125

agc cca tca ctt agg cac aat ctc ttt gag att tta aga gcg cgc cag 432
Ser Pro Ser Leu Arg His Asn Leu Phe Glu Ile Leu Arg Ala Arg Gln
130 135 140

cca tgc ctg tac gcc tgc aac tcg aaa ctg cgc att cga gga cca gca 480
Pro Cys Leu Tyr Ala Cys Asn Ser Lys Leu Arg Ile Arg Gly Pro Ala
145 150 155 160

ggg ccc cta gag agc atg ggc ttg agg tgt cgt tcc ccg gag tga 525
Gly Pro Leu Glu Ser Met Gly Leu Arg Cys Arg Ser Pro Glu *
165 170

<210> 32

<211> 174

<212> PRT

<213> Homo sapiens

<400> 32

Met Gly Val Ser Leu Asp Gln Glu His Ser Arg His Pro Ala Gly Ser
1 5 10 15

Gly Gly Met Gly Val Ser Gly Arg Ser Ala Thr Val Ala Asn Ser Ser
20 25 30

Gly Gly Trp Ile Phe Gly Val Leu Leu Phe Ser Pro Glu Thr Ser Ala

35 40 45
 Ala Ser Gly Ile Phe Ala Gln Val His Val Leu Cys Pro Gly Arg Met
 50 55 60
 Arg Tyr Ala Asp Lys Trp Arg Arg Glu Gly Ser Ala Cys Arg Leu Val
 65 70 75 80
 His Arg Gln Pro Trp Ala Ala Gly Lys Gly Thr Thr Ser Pro His Ser
 85 90 95
 Gly Gln Trp Asn Ser Ser Pro Thr Pro Ser Leu Gln Asp Leu Pro Gly
 100 105 110
 Leu Lys Asn Arg Asn Leu Ala Ala Met Lys Leu Asp Lys Pro Ile Pro
 115 120 125
 Ser Pro Ser Leu Arg His Asn Leu Phe Glu Ile Leu Arg Ala Arg Gln
 130 135 140
 Pro Cys Leu Tyr Ala Cys Asn Ser Lys Leu Arg Ile Arg Gly Pro Ala
 145 150 155 160
 Gly Pro Leu Glu Ser Met Gly Leu Arg Cys Arg Ser Pro Glu
 165 170

<210> 33
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(369)

<400> 33
 atg cgc tcc ctg cat aac gcg cgg cac gcc tcc ttc gct caa ctt ggc 48
 Met Arg Ser Leu His Asn Ala Arg His Ala Ser Phe Ala Gln Leu Gly
 1 5 10 15
 cgt atg ttg att gtc agc atc aac aag ctc cta atg cca cct tta aaa 96
 Arg Met Leu Ile Val Ser Ile Asn Lys Leu Leu Met Pro Pro Leu Lys
 20 25 30
 gtg tct ata tct ctt tta aga tta tta cct cct aca ttt gct gtg ctc 144
 Val Ser Ile Ser Leu Leu Arg Leu Leu Pro Pro Thr Phe Ala Val Leu
 35 40 45
 ttt gta tac aac tcc cgt ttc cgc gct gct tct tac atg caa cac ctc 192
 Phe Val Tyr Asn Ser Arg Phe Arg Ala Ala Ser Tyr Met Gln His Leu
 50 55 60

<210> 35
<211> 1148

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1148)

<400> 35

atg	gag	ccc	ctg	cgc	gcg	ccc	gcg	ctg	cgc	cgc	ctg	ctg	ccg	ccg	ctg	48
Met	Glu	Pro	Leu	Arg	Ala	Pro	Ala	Leu	Arg	Arg	Leu	Leu	Pro	Pro	Leu	
1				5					10					15		

ctg	ctc	ctg	ctg	ctg	tca	ctg	ccc	ccc	cgc	gcc	cgg	gcc	aag	tac	gtg	96
Leu	Leu	Leu	Leu	Leu	Ser	Leu	Pro	Pro	Arg	Ala	Arg	Ala	Lys	Tyr	Val	
				20					25					30		

cgg	ggc	aac	ctc	agt	tcc	aag	gag	gac	tgg	gtg	ttc	ctg	aca	aga	ttt	144
Arg	Gly	Asn	Leu	Ser	Ser	Lys	Glu	Asp	Trp	Val	Phe	Leu	Thr	Arg	Phe	
		35					40					45				

tgt	ttc	ctc	tcg	gat	tac	ggc	cga	ctg	gac	ttc	cgt	ttc	cgc	tac	cct	192
Cys	Phe	Leu	Ser	Asp	Tyr	Gly	Arg	Leu	Asp	Phe	Arg	Phe	Arg	Tyr	Pro	
	50					55					60					

gag	gcc	aag	tgc	tgt	cag	aac	atc	ctc	ctc	tat	ttt	gat	gac	cca	tcc	240
Glu	Ala	Lys	Cys	Cys	Gln	Asn	Ile	Leu	Leu	Tyr	Phe	Asp	Asp	Pro	Ser	
65					70					75					80	

cag	tgg	cca	gcc	gtg	tac	aag	gca	ggg	gac	aag	gac	tgc	ctg	gcc	aag	288
Gln	Trp	Pro	Ala	Val	Tyr	Lys	Ala	Gly	Asp	Lys	Asp	Cys	Leu	Ala	Lys	
				85					90					95		

gag	tca	gtg	atc	cgg	ccg	gag	aac	aac	cag	gtc	atc	aac	ctc	acc	acc	336
Glu	Ser	Val	Ile	Arg	Pro	Glu	Asn	Asn	Gln	Val	Ile	Asn	Leu	Thr	Thr	
			100						105					110		

cag	tat	gcc	tgg	tcc	ggc	tgt	cag	gtg	gta	tca	gag	gag	gga	acc	cgc	384
Gln	Tyr	Ala	Trp	Ser	Gly	Cys	Gln	Val	Val	Ser	Glu	Glu	Gly	Thr	Arg	
		115					120						125			

tac	ctg	agc	tgc	tcc	agt	ggc	cgc	agc	ttc	cgc	tca	gtg	cgt	gaa	cgg	432
Tyr	Leu	Ser	Cys	Ser	Ser	Gly	Arg	Ser	Phe	Arg	Ser	Val	Arg	Glu	Arg	
	130					135					140					

T08290.22330

tgg Trp 145	tgg Trp	tat Tyr	att Ile	gcg Ala	ctc Leu 150	agc Ser	aag Lys	tgt Cys	ggg Gly	ggg Gly 155	gat Asp	gga Gly	ttg Leu	cag Gln	ctg Leu 160	480
gag Glu	tat Tyr	gag Glu	atg Met	gtc Val 165	ctc Leu	acc Thr	aat Asn	ggc Gly	aag Lys 170	tcc Ser	ttc Phe	tgg Trp	aca Thr	cga Arg	cac His 175	528
ttc Phe	tcc Ser	gct Ala	gat Asp 180	gag Glu	ttt Phe	ggg Gly	atc Ile	ctg Leu 185	gag Glu	aca Thr	gat Asp	gtg Val	acc Thr 190	ttc Phe	ctc Leu	576
ctc Leu	atc Ile	ttc Phe 195	atc Ile	ctc Leu	atc Ile	ttc Phe	ttc Phe 200	ctc Leu	tct Ser	tgt Cys	tac Tyr	ttt Phe 205	gga Gly	tat Tyr	ttg Leu	624
ctg Leu 210	aaa Lys	ggg Gly	cgt Arg	cag Gln	ttg Leu	ctc Leu 215	cac His	aca Thr	act Thr	tat Tyr	aaa Lys 220	atg Met	ttc Phe	atg Met	gcc Ala	672
gca Ala 225	gca Ala	gga Gly	gta Val	gag Glu	gtc Val 230	ctg Leu	agc Ser	ctc Leu	cta Leu	ttt Phe 235	ttc Phe	tgc Cys	atc Ile	tac Tyr	tgg Trp 240	720
ggg Gly	caa Gln	tat Tyr	gcc Ala	acc Thr 245	gat Asp	ggc Gly	att Ile	ggc Gly	aac Asn 250	gag Glu	agt Ser	gtg Val	aag Lys	atc Ile 255	ttg Leu	768
gcc Ala	aag Lys	ctg Leu	ctc Leu	ttc Phe	tcc Ser	tcc Ser	agc Ser	ttc Phe 265	ctc Leu	atc Ile	ttc Phe	ctg Leu	ctg Leu 270	atg Met	ctt Leu	816
atc Ile	ctc Leu	ctg Leu	ggg Gly	aag Lys	gga Gly	ttc Phe	acg Thr 280	gtg Val	aca Thr	cgg Arg	tgc Cys	ccg Pro	ggc Gly	agg Arg	gcg Ala	864
tgc Cys 290	tcg Ser	tgg Trp	ggc Gly	ggc Gly	tgg Trp	ggc Gly 295	cgc Arg	atc Ile	agc Ser	cac His	gcg Ala 300	ggc Gly	tcc Ser	gtg Val	aag Lys	912
ttg Leu	tct Ser	gtc Val	tac Tyr	atg Met	acc Thr	ctg Leu	tac Tyr	acg Thr	ctc Leu	acc Thr	cat His	gtg Val	gtg Val	ctg Leu	ctc Leu	960

305 310 315 320

atc tac gag gcg gaa ttc ttt gac cca ggc cag gta ctg tac acg tat 1008
 Ile Tyr Glu Ala Glu Phe Phe Asp Pro Gly Gln Val Leu Tyr Thr Tyr
 325 330 335

gag tcg ccg gcc ggc tac ggg ctc att gga ctg cag gtg gcg gcc tac 1056
 Glu Ser Pro Ala Gly Tyr Gly Leu Ile Gly Leu Gln Val Ala Ala Tyr
 340 345 350

gtg tgg ttc tgc tat gct gtg ctt gtc tca ctg cga cac ttt cct gag 1104
 Val Trp Phe Cys Tyr Ala Val Leu Val Ser Leu Arg His Phe Pro Glu
 355 360 365

aag cag cct ttt tat gtg ccc ttc ttt gct gcc tat acc ctc tg 1148
 Lys Gln Pro Phe Tyr Val Pro Phe Phe Ala Ala Tyr Thr Leu
 370 375 380

<210> 36

<211> 382

<212> PRT

<213> Homo sapiens

<400> 36

Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
 20 25 30
 Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
 35 40 45
 Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
 50 55 60
 Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser
 65 70 75 80
 Gln Trp Pro Ala Val Tyr Lys Ala Gly Asp Lys Asp Cys Leu Ala Lys
 85 90 95
 Glu Ser Val Ile Arg Pro Glu Asn Asn Gln Val Ile Asn Leu Thr Thr
 100 105 110
 Gln Tyr Ala Trp Ser Gly Cys Gln Val Val Ser Glu Glu Gly Thr Arg
 115 120 125
 Tyr Leu Ser Cys Ser Ser Gly Arg Ser Phe Arg Ser Val Arg Glu Arg
 130 135 140

T002290.222550

Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu
 145 150 155 160
 Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His
 165 170 175
 Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu
 180 185 190
 Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu
 195 200 205
 Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala
 210 215 220
 Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Phe Cys Ile Tyr Trp
 225 230 235 240
 Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser Val Lys Ile Leu
 245 250 255
 Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe Leu Leu Met Leu
 260 265 270
 Ile Leu Leu Gly Lys Gly Phe Thr Val Thr Arg Cys Pro Gly Arg Ala
 275 280 285
 Cys Ser Trp Gly Gly Trp Gly Arg Ile Ser His Ala Gly Ser Val Lys
 290 295 300
 Leu Ser Val Tyr Met Thr Leu Tyr Thr Leu Thr His Val Val Leu Leu
 305 310 315 320
 Ile Tyr Glu Ala Glu Phe Phe Asp Pro Gly Gln Val Leu Tyr Thr Tyr
 325 330 335
 Glu Ser Pro Ala Gly Tyr Gly Leu Ile Gly Leu Gln Val Ala Ala Tyr
 340 345 350
 Val Trp Phe Cys Tyr Ala Val Leu Val Ser Leu Arg His Phe Pro Glu
 355 360 365
 Lys Gln Pro Phe Tyr Val Pro Phe Phe Ala Ala Tyr Thr Leu
 370 375 380

<210> 37

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(333)

<400> 37

atg tcg gtg gtt gag gtg caa ggc ctc gtg tgt tat gcg agg cgt ccg
 Met Ser Val Val Glu Val Gln Gly Leu Val Cys Tyr Ala Arg Arg Pro

1	5	10	15	
ctg ata ctt cct ctg ctg ctc ttc tgg tgc ttg agc ggg tct agt cgt				96
Leu Ile Leu Pro Leu Leu Leu Phe Trp Ser Leu Ser Gly Ser Ser Arg				
	20	25	30	
gct act gtc gct act gga cgg tgc cgt agt cgt cgt ata gtg cgt cgt				144
Ala Thr Val Ala Thr Gly Arg Ser Arg Ser Arg Arg Ile Val Arg Arg				
	35	40	45	
gga cct cat gga gat gat agc tac gtg ctt ccg atc gtc gta gat aaa				192
Gly Pro His Gly Asp Asp Ser Tyr Val Leu Pro Ile Val Val Asp Lys				
	50	55	60	
tgg ttg ggc cgt tca ctg acc gtc atc ctc aag cac ggg cta cgg cgg				240
Trp Leu Gly Arg Ser Leu Thr Val Ile Leu Lys His Gly Leu Arg Arg				
	65	70	75	80
ctc gtc gag gac gat aag cac ccg ccc ctc ctc tgg gga tat gtg gct				288
Leu Val Glu Asp Asp Lys His Pro Pro Leu Leu Trp Gly Tyr Val Ala				
	85	90	95	
cca gtg tgg ggg ggc ccc agt gac cca ttt gtt gaa atg ata taa				333
Pro Val Trp Gly Gly Pro Ser Asp Pro Phe Val Glu Met Ile *				
	100	105	110	

<210> 38

<211> 110

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Val Val Glu Val Gln Gly Leu Val Cys Tyr Ala Arg Arg Pro				
1	5	10	15	
Leu Ile Leu Pro Leu Leu Leu Phe Trp Ser Leu Ser Gly Ser Ser Arg				
	20	25	30	
Ala Thr Val Ala Thr Gly Arg Ser Arg Ser Arg Arg Ile Val Arg Arg				
	35	40	45	
Gly Pro His Gly Asp Asp Ser Tyr Val Leu Pro Ile Val Val Asp Lys				
	50	55	60	
Trp Leu Gly Arg Ser Leu Thr Val Ile Leu Lys His Gly Leu Arg Arg				
	65	70	75	80

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<210> 39
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(441)
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<400> 39																
ctg	cag	agc	tat	aga	tcc	aac	tgc	cag	ctg	gac	aaa	ccc	aac	tca	tct	48
Leu	Gln	Ser	Tyr	Arg	Ser	Asn	Cys	Gln	Leu	Asp	Lys	Pro	Asn	Ser	Ser	
1			5			10			15							
cca	gcc	atg	gcc	cct	cct	gat	gga	gca	gcc	ctt	ctg	ctg	ctg	ctg	ctg	96
Pro	Ala	Met	Ala	Pro	Pro	Asp	Gly	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	
			20			25			30							
ctg	ttt	acg	gct	gct	tca	ata	aaa	act	gct	aac	tcc	att	ggc	tcg	ccc	144
Leu	Phe	Thr	Ala	Ala	Ser	Ile	Lys	Thr	Ala	Asn	Ser	Ile	Gly	Ser	Pro	
35						40			45							
tta	cct	tct	ttc	ttg	ggt	gaa	gcc	aca	aac	cct	cct	ggg	agg	cat	gta	192
Leu	Pro	Ser	Phe	Leu	Gly	Glu	Ala	Thr	Asn	Pro	Pro	Gly	Arg	His	Val	
50						55			60							
aag	cgg	tat	ggt	cac	ttt	gaa	gag	cag	ttg	ggt	cac	ttc	tta	aaa	agt	240
Lys	Arg	Tyr	Gly	His	Phe	Glu	Glu	Gln	Leu	Gly	His	Phe	Leu	Lys	Ser	
65			70			75			80							
gaa	acc	tac	tat	atg	acc	cag	tca	ttc	tgc	tcc	tat	gca	cct	cct	caa	288
Glu	Thr	Tyr	Tyr	Met	Thr	Gln	Ser	Phe	Cys	Ser	Tyr	Ala	Pro	Pro	Gln	
			85			90			95							
cag	caa	tgt	ggc	cag	ggt	gcc	cag	gat	gag	tgt	gag	aag	gag	ggc	tgc	336
Gln	Gln	Cys	Gly	Gln	Gly	Ala	Gln	Asp	Glu	Cys	Glu	Lys	Glu	Gly	Cys	
100			105			110			115							

act tcc ctc gag ggg ctg gct gag ctc ctt ggt gct caa tgt cgt acc 432
Thr Ser Leu Glu Gly Leu Ala Glu Leu Leu Gly Ala Gln Cys Arg Thr
130 135 140

att tac tga 441
Ile Tyr *
145

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<210> 40
<211> 146
<212> PRT
<213> Homo sapiens
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[illegible]

<210> 41
<211> 441
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(441)

<400> 41

atg ctg ttg ctg cag ctg ctg ctg ctg ctg ccg ccg ctg ctg ctc ctg	48
Met Leu Leu Leu Gln Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu	
1 5 10 15	
ctt ttt tca gtc tca ctc tgt tgc cca ggc tgg agt gaa gtg ggc atg	96
Leu Phe Ser Val Ser Leu Cys Cys Pro Gly Trp Ser Glu Val Gly Met	
20 25 30	
gaa gtc aaa cca ggt ctc cct tcc cac aac tcg ctg ccc cag ccc atg	144
Glu Val Lys Pro Gly Leu Pro Ser His Asn Ser Leu Pro Gln Pro Met	
35 40 45	
gca gat gga cat ccc cca agg gca tta caa cca tgg cac aag gac acc	192
Ala Asp Gly His Pro Pro Arg Ala Leu Gln Pro Trp His Lys Asp Thr	
50 55 60	
ctt ggt cca gag gga agt tgc aaa gtc tgg ttt gcc tgg aag gag ctc	240
Leu Gly Pro Glu Gly Ser Cys Lys Val Trp Phe Ala Trp Lys Glu Leu	
65 70 75 80	
ttc cag gtg gag gaa gcg gca gat aaa gaa act gaa gtt cag agt gtc	288
Phe Gln Val Glu Glu Ala Ala Asp Lys Glu Thr Glu Val Gln Ser Val	
85 90 95	
agc tta ccc aag gtc aca tct gaa aag cag cag aga cag gtt tca acc	336
Ser Leu Pro Lys Val Thr Ser Glu Lys Gln Gln Arg Gln Val Ser Thr	
100 105 110	
cag att ggg ctg act cca agc ccc atg ctg att ccc tgt ggc acc tgc	384
Gln Ile Gly Leu Thr Pro Ser Pro Met Leu Ile Pro Cys Gly Thr Cys	
115 120 125	
ctc tcg gct ggt aca gaa aac cag gga aag ctg tat ttg aat ctc aac	432
Leu Ser Ala Gly Thr Glu Asn Gln Gly Lys Leu Tyr Leu Asn Leu Asn	
130 135 140	

cca atc tga
Pro Ile *
145

441

<210> 42
<211> 146
<212> PRT
<213> Homo sapiens

<400> 42

Met Leu Leu Leu Gln Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu
1 5 10 15
Leu Phe Ser Val Ser Leu Cys Cys Pro Gly Trp Ser Glu Val Gly Met
20 25 30
Glu Val Lys Pro Gly Leu Pro Ser His Asn Ser Leu Pro Gln Pro Met
35 40 45
Ala Asp Gly His Pro Pro Arg Ala Leu Gln Pro Trp His Lys Asp Thr
50 55 60
Leu Gly Pro Glu Gly Ser Cys Lys Val Trp Phe Ala Trp Lys Glu Leu
65 70 75 80
Phe Gln Val Glu Glu Ala Ala Asp Lys Glu Thr Glu Val Gln Ser Val
85 90 95
Ser Leu Pro Lys Val Thr Ser Glu Lys Gln Gln Arg Gln Val Ser Thr
100 105 110
Gln Ile Gly Leu Thr Pro Ser Pro Met Leu Ile Pro Cys Gly Thr Cys
115 120 125
Leu Ser Ala Gly Thr Glu Asn Gln Gly Lys Leu Tyr Leu Asn Leu Asn
130 135 140
Pro Ile
145

<210> 43
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(203)

<400> 43

atg act ggc tgt ccg gcg tca tca aga cgc cga ggc ttc ggg ctc ttt

48

Met Thr Gly Cys Pro Ala Ser Ser Arg Arg Arg Gly Phe Gly Leu Phe
1 5 10 15

ttc atc ttg cgt cta cac cgc ctc ctg ttg ttg ttt ctg gtt ttg cgt 96
Phe Ile Leu Arg Leu His Arg Leu Leu Leu Phe Leu Val Leu Arg
20 25 30

ggg acc ctg gcc aac aaa ctt aac gtg cca cag gtg ttg cta ccc ttc 144
Gly Thr Leu Ala Asn Lys Leu Asn Val Pro Gln Val Leu Leu Pro Phe
35 40 45

ggc cga gag cca ggc cgg gtg cct ttc ctg ctg gag gcc cag cgg ggc 192
Gly Arg Glu Pro Gly Arg Val Pro Phe Leu Leu Glu Ala Gln Arg Gly
50 55 60

tgc tac act tg 203
Cys Tyr Thr
65

<210> 44

<211> 67

<212> PRT

<213> Homo sapiens

<400> 44

Met Thr Gly Cys Pro Ala Ser Ser Arg Arg Arg Gly Phe Gly Leu Phe
1 5 10 15

Phe Ile Leu Arg Leu His Arg Leu Leu Leu Phe Leu Val Leu Arg
20 25 30

Gly Thr Leu Ala Asn Lys Leu Asn Val Pro Gln Val Leu Leu Pro Phe
35 40 45

Gly Arg Glu Pro Gly Arg Val Pro Phe Leu Leu Glu Ala Gln Arg Gly
50 55 60

Cys Tyr Thr
65

<210> 45

<211> 441

<212> DNA

<213> Homo sapiens

<220>

"42360" 42360

$\langle 222 \rangle \quad (1) \dots (441)$

atg gcc ctg tct tgg ctg gcc ctg tcc ccc ggg tta cag ggc cag aac 48
Met Ala Leu Ser Trp Leu Ala Leu Ser Pro Gly Leu Gln Gly Gln Asn
1 5 10 15

ctg ctg gaa gca ggg cgc agg acc agc cag atc cca cca ggc tcc ctg 96
Leu Leu Glu Ala Gly Arg Arg Thr Ser Gln Ile Pro Pro Gly Ser Leu
20 25 30

agg gac tat aca gtg cct ctg tgc cgc ctg gag ccc agg ccc gcc ttc 144
Arg Asp Tyr Thr Val Pro Leu Cys Arg Leu Glu Pro Arg Pro Ala Phe
35 40 45

tcc gtg gcc gcc ctg gcc ttg agg gcc acc agc ctg gct gcg cag ggc 192
Ser Val Ala Ala Leu Ala Leu Arg Ala Thr Ser Leu Ala Ala Gln Gly
50 55 60

tat gaa gaa ggc atg gaa gac aag gat aac tca ggg aac aga gaa gat 240
Tyr Glu Glu Gly Met Glu Asp Lys Asp Asn Ser Gly Asn Arg Glu Asp
65 70 75 80

ggc agc aca gat agt gtc act tgg ggt ttt gag aaa ggc gat aga tat 288
Gly Ser Thr Asp Ser Val Thr Trp Gly Phe Glu Lys Gly Asp Arg Tyr
85 90 95

tgg ctg cca ctc aga tca tgt ggg ata atg atg cta gaa cag gtt tcc 336
Trp Leu Pro Leu Arg Ser Cys Gly Ile Met Met Leu Glu Gln Val Ser
100 105 110

acc ttc att cat atg cag gag gac ttt gac cag gtt ctc aca gta aat 384
Thr Phe Ile His Met Gln Glu Asp Phe Asp Gln Val Leu Thr Val Asn
115 120 125

atg gaa gaa aaa tct ccc cta gct tct agc agg gga aaa gaa aag gag 432
Met Glu Glu Lys Ser Pro Leu Ala Ser Ser Arg Gly Lys Glu Lys Glu
130 135 140

acc act tag 441
Thr Thr *
145

<210> 46
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Ala Leu Ser Trp Leu Ala Leu Ser Pro Gly Leu Gln Gly Gln Asn
 1 5 10 15
 Leu Leu Glu Ala Gly Arg Arg Thr Ser Gln Ile Pro Pro Gly Ser Leu
 20 25 30
 Arg Asp Tyr Thr Val Pro Leu Cys Arg Leu Glu Pro Arg Pro Ala Phe
 35 40 45
 Ser Val Ala Ala Leu Ala Leu Arg Ala Thr Ser Leu Ala Ala Gln Gly
 50 55 60
 Tyr Glu Glu Gly Met Glu Asp Lys Asp Asn Ser Gly Asn Arg Glu Asp
 65 70 75 80
 Gly Ser Thr Asp Ser Val Thr Trp Gly Phe Glu Lys Gly Asp Arg Tyr
 85 90 95
 Trp Leu Pro Leu Arg Ser Cys Gly Ile Met Met Leu Glu Gln Val Ser
 100 105 110
 Thr Phe Ile His Met Gln Glu Asp Phe Asp Gln Val Leu Thr Val Asn
 115 120 125
 Met Glu Glu Lys Ser Pro Leu Ala Ser Ser Arg Gly Lys Glu Lys Glu
 130 135 140
 Thr Thr
 145

<210> 47
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(384)

<400> 47

atg gta aag ctg ctg ctc tcc ctg ctg tcc aca act ggg gcc tgg agc
 Met Val Lys Leu Leu Ser Leu Leu Ser Thr Thr Gly Ala Trp Ser
 1 5 10 15

tgg ggt cac att tta caa ccg gag ggt tct tgg gag ctg tgg tta cca 96
 Trp Gly His Ile Leu Gln Pro Glu Gly Ser Trp Glu Leu Trp Leu Pro
 20 25 30

ggt tct aca gtg gca ccc act gat cta cag tgg gtg ctc cac cca gga 144
 Gly Ser Thr Val Ala Pro Thr Asp Leu Gln Trp Val Leu His Pro Gly
 35 40 45

ctg ctc agt gag act aat acg ctg cca tcc ttt cta ctg gga act gta 192
 Leu Leu Ser Glu Thr Asn Thr Leu Pro Ser Phe Leu Leu Gly Thr Val
 50 55 60

aca aca cgg act tac tgt gca tcg ggc act gtg cag aga ctt gac att 240
 Thr Thr Arg Thr Tyr Cys Ala Ser Gly Thr Val Gln Arg Leu Asp Ile
 65 70 75 80

agc ctc ctt cag cct tgg ggc tat gag aaa cct tgt ccc att ctg gct 288
 Ser Leu Leu Gln Pro Trp Gly Tyr Glu Lys Pro Cys Pro Ile Leu Ala
 85 90 95

gag ggt gct gaa gta gga agg cgt gtt gga act act gag agc aga gaa 336
 Glu Gly Ala Glu Val Gly Arg Arg Val Gly Thr Thr Glu Ser Arg Glu
 100 105 110

ctc aac aca cac aaa gaa tcc aaa att tgc ttt tac tcg gag tcc tga 384
 Leu Asn Thr His Lys Glu Ser Lys Ile Cys Phe Tyr Ser Glu Ser *
 115 120 125

<210> 48

<211> 127

<212> PRT

<213> Homo sapiens

<400> 48

Met Val Lys Leu Leu Leu Ser Leu Leu Ser Thr Thr Gly Ala Trp Ser
 1 5 10 15
 Trp Gly His Ile Leu Gln Pro Glu Gly Ser Trp Glu Leu Trp Leu Pro
 20 25 30
 Gly Ser Thr Val Ala Pro Thr Asp Leu Gln Trp Val Leu His Pro Gly
 35 40 45
 Leu Leu Ser Glu Thr Asn Thr Leu Pro Ser Phe Leu Leu Gly Thr Val
 50 55 60

Thr Thr Arg Thr Tyr Cys Ala Ser Gly Thr Val Gln Arg Leu Asp Ile
 65 70 75 80
 Ser Leu Leu Gln Pro Trp Gly Tyr Glu Lys Pro Cys Pro Ile Leu Ala
 85 90 95
 Glu Gly Ala Glu Val Gly Arg Arg Val Gly Thr Thr Glu Ser Arg Glu
 100 105 110
 Leu Asn Thr His Lys Glu Ser Lys Ile Cys Phe Tyr Ser Glu Ser
 115 120 125

<210> 49

<211> 1110

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1110)

<400> 49

atg cca ccc atg ctg tgg ctg ctg ctc cac ttt gct gcc ccg gca ctg 48
 Met Pro Pro Met Leu Trp Leu Leu Leu His Phe Ala Ala Pro Ala Leu
 1 5 10 15

ggg ttc tac ttt tcc atc agc tgc ccc agt ggt aag cag tgc caa cag 96
 Gly Phe Tyr Phe Ser Ile Ser Cys Pro Ser Gly Lys Gln Cys Gln Gln
 20 25 30

gcc cta ctc tca ggc aat gat att ctc ctg tat tgc aac tcc tcg ggg 144
 Ala Leu Leu Ser Gly Asn Asp Ile Leu Leu Tyr Cys Asn Ser Ser Gly
 35 40 45

gcg cac tgg tac tat tta ttc aca caa ggc aag aag ggc agg ctc acc 192
 Ala His Trp Tyr Tyr Leu Phe Thr Gln Gly Lys Lys Gly Arg Leu Thr
 50 55 60

agc ctc acc aat att tcc aat atg gaa ata atg ccc gag ggc agc ctt 240
 Ser Leu Thr Asn Ile Ser Asn Met Glu Ile Met Pro Glu Gly Ser Leu
 65 70 75 80

ctc att aaa gat cca ttg ccc tcc cag acg ggc ctc tac cac tgc tgg 288
 Leu Ile Lys Asp Pro Leu Pro Ser Gln Thr Gly Leu Tyr His Cys Trp
 85 90 95

336
384
432
480
528
576
624
672
720
768
816

ggc agg cag ctg cag gtt ttc cag ccg gcc gtc tac aag tgc ttc gtg 864
 Gly Arg Gln Leu Gln Val Phe Gln Pro Ala Val Tyr Lys Cys Phe Val
 275 280 285

 cag cag gag ctc gtg gcc cag ttc aaa ccc gcc gcc agt ctg gag acg 912
 Gln Gln Glu Leu Val Ala Gln Phe Lys Pro Ala Ala Ser Leu Glu Thr
 290 295 300

 ctg gag gct cag tgg aga gag aac gat gcc cag tgg cgg gag gca agg 960
 Leu Glu Ala Gln Trp Arg Glu Asn Asp Ala Gln Trp Arg Glu Ala Arg
 305 310 315 320

 aag gcc ctg cgg ggc agg gcg gac tcc gtg ctc aag ggg ctg aag ctg 1008
 Lys Ala Leu Arg Gly Arg Ala Asp Ser Val Leu Lys Gly Leu Lys Leu
 325 330 335

 gtg ctg ctc gtg gtc acc gtc ctg gcc ctg ctg ggg gcg ctg ctc aag 1056
 Val Leu Leu Val Val Thr Val Leu Ala Leu Leu Gly Ala Leu Leu Lys
 340 345 350

 tgc atc cac cct tcc ccg ggc agg aga agc aca cag gtg ctg gtg gtg 1104
 Cys Ile His Pro Ser Pro Gly Arg Arg Ser Thr Gln Val Leu Val Val
 355 360 365

 aaa taa 1110
 Lys *

<210> 50

<211> 369

<212> PRT

<213> Homo sapiens

<400> 50

Met Pro Pro Met Leu Trp Leu Leu Leu His Phe Ala Ala Pro Ala Leu
 1 5 10 15
 Gly Phe Tyr Phe Ser Ile Ser Cys Pro Ser Gly Lys Gln Cys Gln Gln
 20 25 30
 Ala Leu Leu Ser Gly Asn Asp Ile Leu Leu Tyr Cys Asn Ser Ser Gly
 35 40 45
 Ala His Trp Tyr Tyr Leu Phe Thr Gln Gly Lys Lys Gly Arg Leu Thr

50 55 60
 Ser Leu Thr Asn Ile Ser Asn Met Glu Ile Met Pro Glu Gly Ser Leu
 65 70 75 80
 Leu Ile Lys Asp Pro Leu Pro Ser Gln Thr Gly Leu Tyr His Cys Trp
 85 90 95
 Asn Lys Asn Gly Arg Gln Val Val Gln Tyr Glu Ile Asp Phe Gln Asp
 100 105 110
 Val Thr Thr Leu His Ile Thr His Lys Asp Leu Gly Gln Arg Pro Leu
 115 120 125
 Gln Asn Glu Thr Leu His Leu Gly Ser Lys Gln Leu Ile Phe Thr Trp
 130 135 140
 Trp Glu Pro Trp Gln Asp Cys Asn Arg Cys Glu Glu Pro Gly Glu Cys
 145 150 155 160
 Lys Arg Leu Gly Tyr Arg Tyr Ile Glu Glu Pro Leu Glu Glu Ala Met
 165 170 175
 Pro Cys Trp Leu Tyr Leu Gly Glu Val Leu Val Trp Ser Ser Arg Leu
 180 185 190
 Arg Pro Glu Leu Gln Val Glu Ala Cys His Val Gln Cys Thr Asn Asn
 195 200 205
 Thr Gln Leu Arg Val Asp Tyr Val Ile Phe Asp Asn Phe Arg Leu Asp
 210 215 220
 Glu Lys Thr Glu Phe Val Trp Leu Asp Cys Pro Leu Gly Ser Met Tyr
 225 230 235 240
 Arg Pro Val Asn Trp Arg Ala Asn Asp Thr Pro Leu Thr Trp Glu Ser
 245 250 255
 Gln Leu Ser Gly Gln Asp Phe Thr Thr Phe Leu Asp Pro Ser Thr Gly
 260 265 270
 Gly Arg Gln Leu Gln Val Phe Gln Pro Ala Val Tyr Lys Cys Phe Val
 275 280 285
 Gln Gln Glu Leu Val Ala Gln Phe Lys Pro Ala Ala Ser Leu Glu Thr
 290 295 300
 Leu Glu Ala Gln Trp Arg Glu Asn Asp Ala Gln Trp Arg Glu Ala Arg
 305 310 315 320
 Lys Ala Leu Arg Gly Arg Ala Asp Ser Val Leu Lys Gly Leu Lys Leu
 325 330 335
 Val Leu Leu Val Val Thr Val Leu Ala Leu Leu Gly Ala Leu Leu Lys
 340 345 350
 Cys Ile His Pro Ser Pro Gly Arg Arg Ser Thr Gln Val Leu Val Val
 355 360 365
 Lys

<211> 759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(759)

<400> 51

atg gca gcc ccc gcc ctg ctg ctc cta gca ctg ctg ctg ccc gtg ggg	48
Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1 5 10 15	
gcc tgg ccc ggg ctg ccc agg agg ccc tgt gtg cac tgc tgc cgc ccg	96
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
20 25 30	
gcc tgg ccc cct gga ccc tat gcc cgg gtg agt gac agg gac ctg tgg	144
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
35 40 45	
agg ggg gac ctg tgg agg ggg ctg cct cga gta cgg ccc act ata gac	192
Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp	
50 55 60	
atc gaa atc ctc aaa ggt gag aag ggt gag gcc ggc gtc cga ggt cgg	240
Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg	
65 70 75 80	
gcc ggc agg agc ggg aaa gag ggg ccg cca ggc gcc cgg ggc ctg cag	288
Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln	
85 90 95	
ggc cgc aga ggc cag aag ggg cag gtg ggg ccg ccg ggc gcc gcg tgc	336
Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys	
100 105 110	
cga cgt gcc tac gcc gcc ttc tcc gtg ggc cgg cgc gag ggc ctg cac	384
Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His	
115 120 125	
agc tcc gac cac ttc cag gcg gtg ccc ttc gac acg gag ctg gtg aac	432
Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn	

130	135	140	
ctg gac ggc gcc ttc gac	ctg gcc gcg ggc cgc ttc ctc tgc acg gtg		480
Leu Asp Gly Ala Phe Asp	Leu Ala Ala Gly Arg Phe Leu Cys Thr Val		
145	150	155	160
ccc ggc gtc tac ttc ctc agc ctc aac gtg cac acc tgg aac tac aag			528
Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys			
	165	170	175
gag acc tac ctg cac atc atg ctg aac cgg cgg ccc gcg gcc gtg ctc			576
Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu			
	180	185	190
tac gcg cag ccc agc gag cgc agc gtc atg cag gcc cag agc ctg atg			624
Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met			
	195	200	205
ctg ctg ctg gcg gcg ggc gac gcc gtc tgg gtg cgc atg ttc cag cgc			672
Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg			
	210	215	220
gac cgg gac aac gcc atc tac ggc gag cac gga gac ctc tac atc acc			720
Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr			
	225	230	235
ttc agc ggc cac ctg gtc aag ccg gcc gcc gag ctg tag			759
Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu *			
	245	250	

<210> 52

<211> 252

<212> PRT

<213> Homo sapiens

<400> 52

Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1	15
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
20	30
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
35	45

Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp
 50 55 60
 Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg
 65 70 75 80
 Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln
 85 90 95
 Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys
 100 105 110
 Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His
 115 120 125
 Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn
 130 135 140
 Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val
 145 150 155 160
 Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys
 165 170 175
 Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu
 180 185 190
 Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met
 195 200 205
 Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg
 210 215 220
 Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr
 225 230 235 240
 Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu
 245 250

<210> 53

<211> 293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(293)

<400> 53

atg cag gcc ccc tcg ctc ctc agc gtg gtg gcc gtc tgg ctg acc tgg 48
 Met Gln Ala Pro Ser Leu Leu Ser Val Val Ala Val Trp Leu Thr Trp
 1 5 10 15

gcc aat ggg gcc atc aac cct gtc atc tac gcc atc cgc aat ccc aac 96
 Ala Asn Gly Ala Ile Asn Pro Val Ile Tyr Ala Ile Arg Asn Pro Asn

	20	25	30	
att tcg atg ctc cta ggg cgc aac cgc gag gag ggc tac cgg act agg				144
Ile Ser Met Leu Leu Gly Arg Asn Arg Glu Glu Gly Tyr Arg Thr Arg				
	35	40	45	
aat gtg gac gct ttc ctg ccc agc cag ggc ccg ggt ctg caa gcc aga				192
Asn Val Asp Ala Phe Leu Pro Ser Gln Gly Pro Gly Leu Gln Ala Arg				
	50	55	60	
agc cgc agt cgc ctt cga aac cgc tat gcc aac cgg ctg ggg gcc tgc				240
Ser Arg Ser Arg Leu Arg Asn Arg Tyr Ala Asn Arg Leu Gly Ala Cys				
	65	70	75	80
aac agg atg tcc tct tcc aac ccg gcc agc gga gtg gca ggg gac gtg				288
Asn Arg Met Ser Ser Ser Asn Pro Ala Ser Gly Val Ala Gly Asp Val				
	85	90	95	
gcc at				293
Ala				

<210> 54

<211> 97

<212> PRT

<213> Homo sapiens

<400> 54

Met Gln Ala Pro Ser Leu Leu Ser Val Val Ala Val Trp Leu Thr Trp				
1	5	10	15	
Ala Asn Gly Ala Ile Asn Pro Val Ile Tyr Ala Ile Arg Asn Pro Asn				
	20	25	30	
Ile Ser Met Leu Leu Gly Arg Asn Arg Glu Glu Gly Tyr Arg Thr Arg				
	35	40	45	
Asn Val Asp Ala Phe Leu Pro Ser Gln Gly Pro Gly Leu Gln Ala Arg				
	50	55	60	
Ser Arg Ser Arg Leu Arg Asn Arg Tyr Ala Asn Arg Leu Gly Ala Cys				
	65	70	75	80
Asn Arg Met Ser Ser Ser Asn Pro Ala Ser Gly Val Ala Gly Asp Val				
	85	90	95	
Ala				

<210> 55
 <211> 258
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(258)

<400> 55

atg tca ccg ccg ccg ccg ctg ctg ctg ctg ctg ctg ctg agt ctg gcg	48
Met Ser Pro Pro Pro Pro Leu Leu Leu Leu Leu Leu Leu Ser Leu Ala	
1 5 10 15	
ctg ctg ggc gcc cgg gcc cgc gcc gag ccc gcc ggg agt gcc gtc ccc	96
Leu Leu Gly Ala Arg Ala Arg Ala Glu Pro Ala Gly Ser Ala Val Pro	
20 25 30	
gcg cag agc cgc cca tgc gtg gac tgc cac gcc ttc gag ttc atg cag	144
Ala Gln Ser Arg Pro Cys Val Asp Cys His Ala Phe Glu Phe Met Gln	
35 40 45	
cgc gcc ctg cag gac ctg cgg aag aca gcc tgc agc ctg gac gcg cgg	192
Arg Ala Leu Gln Asp Leu Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg	
50 55 60	
acg gag acc cta ctg ctg cag gca gag cgc cgt gcc ctg tgt gcc tgc	240
Thr Glu Thr Leu Leu Leu Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys	
65 70 75 80	
tgg cca gcg ggg cac tga	258
Trp Pro Ala Gly His *	
85	

<210> 56
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 56

Met Ser Pro Pro Pro Pro Leu Leu Leu Leu Leu Leu Ser Leu Ala

1 5 10 15
 Leu Leu Gly Ala Arg Ala Arg Ala Glu Pro Ala Gly Ser Ala Val Pro
 20 25 30
 Ala Gln Ser Arg Pro Cys Val Asp Cys His Ala Phe Glu Phe Met Gln
 35 40 45
 Arg Ala Leu Gln Asp Leu Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg
 50 55 60
 Thr Glu Thr Leu Leu Leu Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys
 65 70 75 80
 Trp Pro Ala Gly His
 85

<210> 57
 <211> 570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(570)

<400> 57

atg gag gaa caa gcc aca cag ggg gtt cca aag tct cca ggg gat gct	48
Met Glu Glu Gln Ala Thr Gln Gly Val Pro Lys Ser Pro Gly Asp Ala	
1 5 10 15	
 gag gaa gcc ttc ctt gcc ctg tcc tgg gtc ttg gcc agc ggt ggg ctc	96
Glu Glu Ala Phe Leu Ala Leu Ser Trp Val Leu Ala Ser Gly Gly Leu	
20 25 30	
 ccc agg gac ctc acc agg acg gca ttt tgc gag agc cga agc cgg aag	144
Pro Arg Asp Leu Thr Arg Thr Ala Phe Cys Glu Ser Arg Ser Arg Lys	
35 40 45	
 cgg cct cgg ggt gcg ctg cac cgc ctc ttc cgg ggc ctc tct agg ccg	192
Arg Pro Arg Gly Ala Leu His Arg Leu Phe Arg Gly Leu Ser Arg Pro	
50 55 60	
 gag cgc ggg att tcg gtg gcc ggg aga ggc cgg aac ggc ttc gcg ggg	240
Glu Arg Gly Ile Ser Val Ala Gly Arg Gly Arg Asn Gly Phe Ala Gly	
65 70 75 80	
 cag cgg cgc ctc ctg gcg ggc ctg ggg tca ggc agt ccg tgg ggg gtc	288

Gln Arg Arg Leu Leu Ala Gly Leu Gly Ser Gly Ser Pro Trp Gly Val
 85 90 95

tgg ctg gct ccc tgc agt aca cac ctg cgc cga tgc cca gcg ttg agg 336
 Trp Leu Ala Pro Cys Ser Thr His Leu Arg Arg Cys Pro Ala Leu Arg
 100 105 110

ccc tac cca tcc cgg ggg acc ttt ccc ctc ccg cct ccc gcc ctt ctg 384
 Pro Tyr Pro Ser Arg Gly Thr Phe Pro Leu Pro Pro Pro Ala Leu Leu
 115 120 125

tcg gct ttc ttc cca cgg atc tgc cag gaa gcc ttc cag gac tgt cct 432
 Ser Ala Phe Phe Pro Arg Ile Cys Gln Glu Ala Phe Gln Asp Cys Pro
 130 135 140

gga gca tca agg ctc gac cgc acg gcc atg ggt acc gac cat ccc agc 480
 Gly Ala Ser Arg Leu Asp Arg Thr Ala Met Gly Thr Asp His Pro Ser
 145 150 155 160

cac acg gct ggg caa cgt gtg gtg ggt cac cgc gca gcc aga ctc cgg 528
 His Thr Ala Gly Gln Arg Val Val Gly His Arg Ala Ala Arg Leu Arg
 165 170 175

ctg gtg acc gcc agg ggt cag cag agg cct cct ttt gca tag 570
 Leu Val Thr Ala Arg Gly Gln Gln Arg Pro Pro Phe Ala *
 180 185

<210> 58

<211> 189

<212> PRT

<213> Homo sapiens

<400> 58

Met Glu Glu Gln Ala Thr Gln Gly Val Pro Lys Ser Pro Gly Asp Ala
 1 5 10 15
 Glu Glu Ala Phe Leu Ala Leu Ser Trp Val Leu Ala Ser Gly Gly Leu
 20 25 30
 Pro Arg Asp Leu Thr Arg Thr Ala Phe Cys Glu Ser Arg Ser Arg Lys
 35 40 45
 Arg Pro Arg Gly Ala Leu His Arg Leu Phe Arg Gly Leu Ser Arg Pro
 50 55 60
 Glu Arg Gly Ile Ser Val Ala Gly Arg Gly Arg Asn Gly Phe Ala Gly

65 70 75 80
 Gln Arg Arg Leu Leu Ala Gly Leu Gly Ser Gly Ser Pro Trp Gly Val
 85 90 95
 Trp Leu Ala Pro Cys Ser Thr His Leu Arg Arg Cys Pro Ala Leu Arg
 100 105 110
 Pro Tyr Pro Ser Arg Gly Thr Phe Pro Leu Pro Pro Pro Ala Leu Leu
 115 120 125
 Ser Ala Phe Phe Pro Arg Ile Cys Gln Glu Ala Phe Gln Asp Cys Pro
 130 135 140
 Gly Ala Ser Arg Leu Asp Arg Thr Ala Met Gly Thr Asp His Pro Ser
 145 150 155 160
 His Thr Ala Gly Gln Arg Val Val Gly His Arg Ala Ala Arg Leu Arg
 165 170 175
 Leu Val Thr Ala Arg Gly Gln Gln Arg Pro Pro Phe Ala
 180 185

<210> 59
 <211> 498
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(498)

<400> 59
 atg aga aag ata ctt ttc cta aac ctg tgg atc tca cta gtg aaa gca 48
 Met Arg Lys Ile Leu Phe Leu Asn Leu Trp Ile Ser Leu Val Lys Ala
 1 5 10 15

 agc aca tac cag gga gaa cag gaa gcc aga ggc acc aac aac act gag 96
 Ser Thr Tyr Gln Gly Glu Gln Glu Ala Arg Gly Thr Asn Asn Thr Glu
 20 25 30

 ttt gat gca aaa aag ggg gac ttt agt tca ggc tgc ata aaa aca gga 144
 Phe Asp Ala Lys Lys Gly Asp Phe Ser Ser Gly Cys Ile Lys Thr Gly
 35 40 45

 ggc cga ttc aat gca tgg ata aac ggg tct gtc tac ctc cat cgc cgc 192
 Gly Arg Phe Asn Ala Trp Ile Asn Gly Ser Val Tyr Leu His Arg Arg
 50 55 60

 tcg tca agt gca atg gga acc gat gaa aca ctg aag gcc tct ggg ctg 240

Ser Ser Ser Ala Met Gly Thr Asp Glu Thr Leu Lys Ala Ser Gly Leu
 65 70 75 80
 gcg tca acc gaa gag aca ccg gcc aag cac agt gac cgc aac cgg ctg 288
 Ala Ser Thr Glu Glu Thr Pro Ala Lys His Ser Asp Arg Asn Arg Leu
 85 90 95
 gaa caa acc cca cgg gac cca gag tgg gac cag gcc tgg ggg cgc aag 336
 Glu Gln Thr Pro Arg Asp Pro Glu Trp Asp Gln Ala Trp Gly Arg Lys
 100 105 110
 gag gcc cgg ctg cca tcc gtc gca tgc gca aag gag ggg ctc acc caa 384
 Glu Ala Arg Leu Pro Ser Val Ala Cys Ala Lys Glu Gly Leu Thr Gln
 115 120 125
 caa acg ata tgc agc gcc gcg gtt tct gcg ccg ctg gtc ccc acg gtg 432
 Gln Thr Ile Cys Ser Ala Ala Val Ser Ala Pro Leu Val Pro Thr Val
 130 135 140
 gag tca cac acg cag tcc gtt gac cct gta aag gga aaa aga agg tcc 480
 Glu Ser His Thr Gln Ser Val Asp Pro Val Lys Gly Lys Arg Arg Ser
 145 150 155 160
 caa ata gca tca gaa taa 498
 Gln Ile Ala Ser Glu *
 165

<210> 60

<211> 165

<212> PRT

<213> Homo sapiens

<400> 60

Met Arg Lys Ile Leu Phe Leu Asn Leu Trp Ile Ser Leu Val Lys Ala
 1 5 10 15
 Ser Thr Tyr Gln Gly Glu Gln Glu Ala Arg Gly Thr Asn Asn Thr Glu
 20 25 30
 Phe Asp Ala Lys Lys Gly Asp Phe Ser Ser Gly Cys Ile Lys Thr Gly
 35 40 45
 Gly Arg Phe Asn Ala Trp Ile Asn Gly Ser Val Tyr Leu His Arg Arg
 50 55 60
 Ser Ser Ser Ala Met Gly Thr Asp Glu Thr Leu Lys Ala Ser Gly Leu

65 70 75 80
 Ala Ser Thr Glu Glu Thr Pro Ala Lys His Ser Asp Arg Asn Arg Leu
 85 90 95
 Glu Gln Thr Pro Arg Asp Pro Glu Trp Asp Gln Ala Trp Gly Arg Lys
 100 105 110
 Glu Ala Arg Leu Pro Ser Val Ala Cys Ala Lys Glu Gly Leu Thr Gln
 115 120 125
 Gln Thr Ile Cys Ser Ala Ala Val Ser Ala Pro Leu Val Pro Thr Val
 130 135 140
 Glu Ser His Thr Gln Ser Val Asp Pro Val Lys Gly Lys Arg Arg Ser
 145 150 155 160
 Gln Ile Ala Ser Glu
 165

<210> 61
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(462)

<400> 61
 atg cac ctg cgg ctg cta cca cta ctg ctt ctg cta atg ctg tcg tta 48
 Met His Leu Arg Leu Leu Pro Leu Leu Leu Leu Leu Met Leu Ser Leu
 1 5 10 15

 aaa ctg atg gct acc acg cgt ggt cga tta tgt gct acg tct tgt gca 96
 Lys Leu Met Ala Thr Thr Arg Gly Arg Leu Cys Ala Thr Ser Cys Ala
 20 25 30

 aga ctc caa gtt ctt cag tgt cga act ctt gga ctt aca cca gtg gtt 144
 Arg Leu Gln Val Leu Gln Cys Arg Thr Leu Gly Leu Thr Pro Val Val
 35 40 45

 tgc cag cgg ctc tcg agc ctt ctg cta cag act gaa ggc tac gct ctc 192
 Cys Gln Arg Leu Ser Ser Leu Leu Leu Gln Thr Glu Gly Tyr Ala Leu
 50 55 60

 ggc ttc cct act ttt agg gct ttg gga ctt gaa ctg gct tcc ttg ctc 240
 Gly Phe Pro Thr Phe Arg Ala Leu Gly Leu Glu Leu Ala Ser Leu Leu
 65 70 75 80

ctc agc ttg cag atg gcc tat tgt ggg act tta cct tgt gat cat aat 288
 Leu Ser Leu Gln Met Ala Tyr Cys Gly Thr Leu Pro Cys Asp His Asn
 85 90 95

gct acg ctg tca cct gca gga aag cct gag cag ata aag atg gct tct 336
 Ala Thr Leu Ser Pro Ala Gly Lys Pro Glu Gln Ile Lys Met Ala Ser
 100 105 110

gca cct gga gga aat ggg aat ttc cag cga gac agg aag aaa atg att 384
 Ala Pro Gly Gly Asn Gly Asn Phe Gln Arg Asp Arg Lys Lys Met Ile
 115 120 125

caa aat ttg aaa gct ata agt gac cac att att ccc act gca tat gaa 432
 Gln Asn Leu Lys Ala Ile Ser Asp His Ile Ile Pro Thr Ala Tyr Glu
 130 135 140

gaa att gat gca cag gaa ata aac gtt tga 462
 Glu Ile Asp Ala Gln Glu Ile Asn Val *
 145 150

<210> 62

<211> 153

<212> PRT

<213> Homo sapiens

<400> 62

Met His Leu Arg Leu Leu Pro Leu Leu Leu Leu Met Leu Ser Leu
 1 5 10 15
 Lys Leu Met Ala Thr Thr Arg Gly Arg Leu Cys Ala Thr Ser Cys Ala
 20 25 30
 Arg Leu Gln Val Leu Gln Cys Arg Thr Leu Gly Leu Thr Pro Val Val
 35 40 45
 Cys Gln Arg Leu Ser Ser Leu Leu Leu Gln Thr Glu Gly Tyr Ala Leu
 50 55 60
 Gly Phe Pro Thr Phe Arg Ala Leu Gly Leu Glu Leu Ala Ser Leu Leu
 65 70 75 80
 Leu Ser Leu Gln Met Ala Tyr Cys Gly Thr Leu Pro Cys Asp His Asn
 85 90 95
 Ala Thr Leu Ser Pro Ala Gly Lys Pro Glu Gln Ile Lys Met Ala Ser
 100 105 110
 Ala Pro Gly Gly Asn Gly Asn Phe Gln Arg Asp Arg Lys Lys Met Ile

115 120 125
 Gln Asn Leu Lys Ala Ile Ser Asp His Ile Ile Pro Thr Ala Tyr Glu
 130 135 140
 Glu Ile Asp Ala Gln Glu Ile Asn Val
 145 150

<210> 63
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(315)

<400> 63

atg aag gtt gga gga ctc agc aag aca gct ttt tct tct acc ttc ttc 48
 Met Lys Val Gly Gly Leu Ser Lys Thr Ala Phe Ser Ser Thr Phe Phe
 1 5 10 15

tcc ctg ctt ttt cca gcc tca ctg gca gct gat tgg atg gtg ccc acc 96
 Ser Leu Leu Phe Pro Ala Ser Leu Ala Ala Asp Trp Met Val Pro Thr
 20 25 30

aca ttg tgg aca tta gaa cta aag ttt ctt ggg cct tta gac ttg agg 144
 Thr Leu Trp Thr Leu Glu Leu Lys Phe Leu Gly Pro Leu Asp Leu Arg
 35 40 45

gct tac atc agt ggc ccc caa ttt ctc aaa ctt tca act tca aat aaa 192
 Ala Tyr Ile Ser Gly Pro Gln Phe Leu Lys Leu Ser Thr Ser Asn Lys
 50 55 60

gtt aca tcc tca gat ccc cca ggt tct tct ttg gac tca gac tgg att 240
 Val Thr Ser Ser Asp Pro Pro Gly Ser Ser Leu Asp Ser Asp Trp Ile
 65 70 75 80

aca tca aaa gct ttc ctg gtt ctt cag ttt gaa gac agc atg ttg tgg 288
 Thr Ser Lys Ala Phe Leu Val Leu Gln Phe Glu Asp Ser Met Leu Trp
 85 90 95

gac ttc tca acc tct ata att gtg tga 315
 Asp Phe Ser Thr Ser Ile Ile Val *
 100

<210> 64
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 64

Met Lys Val Gly Gly Leu Ser Lys Thr Ala Phe Ser Ser Thr Phe Phe
 1 5 10 15
 Ser Leu Leu Phe Pro Ala Ser Leu Ala Ala Asp Trp Met Val Pro Thr
 20 25 30
 Thr Leu Trp Thr Leu Glu Leu Lys Phe Leu Gly Pro Leu Asp Leu Arg
 35 40 45
 Ala Tyr Ile Ser Gly Pro Gln Phe Leu Lys Leu Ser Thr Ser Asn Lys
 50 55 60
 Val Thr Ser Ser Asp Pro Pro Gly Ser Ser Leu Asp Ser Asp Trp Ile
 65 70 75 80
 Thr Ser Lys Ala Phe Leu Val Leu Gln Phe Glu Asp Ser Met Leu Trp
 85 90 95
 Asp Phe Ser Thr Ser Ile Ile Val
 100

<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(339)

<400> 65

atg tgg gat gaa tca agt aca acc aca tgt gtt cca aag gtc aat gag 48
 Met Trp Asp Glu Ser Ser Thr Thr Thr Cys Val Pro Lys Val Asn Glu
 1 5 10 15
 agg ctc ttc gtg ctt tta gca tta att ttg cct cca ttg aca tca gag 96
 Arg Leu Phe Val Leu Leu Ala Leu Ile Leu Pro Pro Leu Thr Ser Glu
 20 25 30
 att ctg gat aac aac cgc ctc aga caa ata ttt gta gtg ttt ggc cct 144
 Ile Leu Asp Asn Asn Arg Leu Arg Gln Ile Phe Val Val Phe Gly Pro

35	40	45	
cac aat ctt ctg caa gca gtt ggc cag aag aaa cac ata aaa cac aga			192
His Asn Leu Leu Gln Ala Val Gly Gln Lys Lys His Ile Lys His Arg			
50	55	60	
aca cag acg tat ctg gtc ttt tca gaa aca gca aat aga gag cca ctg			240
Thr Gln Thr Tyr Leu Val Phe Ser Glu Thr Ala Asn Arg Glu Pro Leu			
65	70	75	80
aaa act ggc tcc ctt ggg gct ctg caa gaa aca gct agc acc tct ggc			288
Lys Thr Gly Ser Leu Gly Ala Leu Gln Glu Thr Ala Ser Thr Ser Gly			
	85	90	95
gat gga ggc cag cca cac ctc act acc ttg aaa agt agg gta act cag			336
Asp Gly Gly Gln Pro His Leu Thr Thr Leu Lys Ser Arg Val Thr Gln			
	100	105	110
tag			339
*			

<210> 66
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 66

Met Trp Asp Glu Ser Ser Thr Thr Thr Cys Val Pro Lys Val Asn Glu			
1	5	10	15
Arg Leu Phe Val Leu Leu Ala Leu Ile Leu Pro Pro Leu Thr Ser Glu			
	20	25	30
Ile Leu Asp Asn Asn Arg Leu Arg Gln Ile Phe Val Val Phe Gly Pro			
	35	40	45
His Asn Leu Leu Gln Ala Val Gly Gln Lys Lys His Ile Lys His Arg			
	50	55	60
Thr Gln Thr Tyr Leu Val Phe Ser Glu Thr Ala Asn Arg Glu Pro Leu			
65	70	75	80
Lys Thr Gly Ser Leu Gly Ala Leu Gln Glu Thr Ala Ser Thr Ser Gly			
	85	90	95
Asp Gly Gly Gln Pro His Leu Thr Thr Leu Lys Ser Arg Val Thr Gln			
	100	105	110

<400> 67

<400> 68

Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val

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<210> 69
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(357)
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<400> 69																
atg	ggc	tca	aag	aag	gta	gaa	ggg	ttg	ggt	ccg	gac	gaa	ctg	ctg	ctg	48
Met	Gly	Ser	Lys	Lys	Val	Glu	Gly	Leu	Gly	Pro	Asp	Glu	Leu	Leu	Leu	
1			5			10			15							
tta	ctg	ttg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	96
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
20				25				30								
tcc	agc	agg	gca	gaa	gac	tgc	agt	ggc	cgg	gtg	tcc	agt	gtt	gtt	ggg	144
Ser	Ser	Arg	Ala	Glu	Asp	Cys	Ser	Gly	Arg	Val	Ser	Ser	Val	Val	Gly	
35			40			45										
ccc	agt	ggg	agt	gaa	ctg	agc	tca	cca	ctg	tcc	ttg	cta	tca	gtc	cca	192
Pro	Ser	Gly	Ser	Glu	Leu	Ser	Ser	Pro	Leu	Ser	Leu	Leu	Ser	Val	Pro	
50			55			60										
ggg	ccg	cca	ctc	act	aca	atg	ata	gcc	ccc	aaa	ccc	agt	cat	aca	aga	240
Gly	Pro	Pro	Leu	Thr	Thr	Met	Ile	Ala	Pro	Lys	Pro	Ser	His	Thr	Arg	
65			70			75			80							
gga	agt	aac	ctg	aaa	tta	gtc	acc	aca	gga	gac	agg	gac	aca	aga	cct	288

Gly Ser Asn Leu Lys Leu Val Thr Thr Gly Asp Arg Asp Thr Arg Pro
 85 90 95

aca gaa gaa gac tcg tgg tca aca tgt ctg ctg tgg cca tac ttc aag 336
 Thr Glu Glu Asp Ser Trp Ser Thr Cys Leu Leu Trp Pro Tyr Phe Lys
 100 105 110

acg ggc tac cag ggc aat tga 357
 Thr Gly Tyr Gln Gly Asn *
 115

<210> 70
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Gly Ser Lys Lys Val Glu Gly Leu Gly Pro Asp Glu Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
 20 25 30
 Ser Ser Arg Ala Glu Asp Cys Ser Gly Arg Val Ser Ser Val Val Gly
 35 40 45
 Pro Ser Gly Ser Glu Leu Ser Ser Pro Leu Ser Leu Leu Ser Val Pro
 50 55 60
 Gly Pro Pro Leu Thr Thr Met Ile Ala Pro Lys Pro Ser His Thr Arg
 65 70 75 80
 Gly Ser Asn Leu Lys Leu Val Thr Thr Gly Asp Arg Asp Thr Arg Pro
 85 90 95
 Thr Glu Glu Asp Ser Trp Ser Thr Cys Leu Leu Trp Pro Tyr Phe Lys
 100 105 110
 Thr Gly Tyr Gln Gly Asn
 115

<210> 71
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(474)

<400> 71																
atg	aag	gca	gcc	tgc	tct	tcc	ctc	tgc	ttg	tca	ctg	ttg	gct	tta	gaa	48
Met	Lys	Ala	Ala	Cys	Ser	Ser	Leu	Cys	Leu	Ser	Leu	Leu	Ala	Leu	Glu	
1				5					10					15		
gcc	acc	tgg	gga	tta	gga	gca	gca	ggt	gac	aag	cac	ttt	gaa	gat	gcc	96
Ala	Thr	Trp	Gly	Leu	Gly	Ala	Ala	Gly	Asp	Lys	His	Phe	Glu	Asp	Ala	
			20					25					30			
ctc	cca	gtg	tcg	ggg	ctg	gct	cct	gat	gtg	cag	tgt	cgg	cac	ctc	ggc	144
Leu	Pro	Val	Ser	Gly	Leu	Ala	Pro	Asp	Val	Gln	Cys	Arg	His	Leu	Gly	
			35				40					45				
act	tgg	ggc	gac	tgt	tgt	ggc	tgt	gct	gat	ttg	ctc	atg	atg	cgc	cac	192
Thr	Trp	Gly	Asp	Cys	Cys	Gly	Cys	Ala	Asp	Leu	Leu	Met	Met	Arg	His	
	50					55					60					
gac	ctg	gac	tcc	agt	tac	ttg	cac	gtg	gga	tcc	cct	gct	gtc	gtc	cgc	240
Asp	Leu	Asp	Ser	Ser	Tyr	Leu	His	Val	Gly	Ser	Pro	Ala	Val	Val	Arg	
65					70					75					80	
aag	tca	ccg	agg	ggg	tgt	gga	gga	gcc	ttg	cct	gac	agc	cgg	agg	gag	288
Lys	Ser	Pro	Arg	Gly	Cys	Gly	Gly	Ala	Leu	Pro	Asp	Ser	Arg	Arg	Glu	
				85					90					95		
ctg	gag	tct	gaa	atg	tca	gct	gct	ctt	ttt	aca	gaa	cgt	tat	gtc	aca	336
Leu	Glu	Ser	Glu	Met	Ser	Ala	Ala	Leu	Phe	Thr	Glu	Arg	Tyr	Val	Thr	
			100					105					110			
ggc	ctt	caa	ata	aga	gcg	ccc	aat	ttc	ggc	tca	aga	cgc	gca	ctg	agc	384
Gly	Leu	Gln	Ile	Arg	Ala	Pro	Asn	Phe	Gly	Ser	Arg	Arg	Ala	Leu	Ser	
		115					120					125				
aga	gat	atg	gag	ctg	gcc	ctg	acc	acg	ctg	tgg	agc	ccg	tgc	tgg	tcc	432
Arg	Asp	Met	Glu	Leu	Ala	Leu	Thr	Thr	Leu	Trp	Ser	Pro	Cys	Trp	Ser	
	130					135					140					
ctc	aag	cct	cca	gcc	acc	tgc	acg	cgg	ggc	cag	cca	ggc	cag			474
Leu	Lys	Pro	Pro	Ala	Thr	Cys	Thr	Arg	Gly	Gln	Pro	Gly	Gln			
145					150					155						

<400> 72

<210> 73

<212> DNA

<213> Home

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (411)$

<400> 73

48

96

20	25	30	
cag gca tgc cag ccc gat tca cac tcg gct cag aga cct ctg acc caa			144
Gln Ala Cys Gln Pro Asp Ser His Ser Ala Gln Arg Pro Leu Thr Gln			
35	40	45	
tta ccc ctg gtt cct ggt gag cct cgc tgc aag acg gaa gcc tgt cac			192
Leu Pro Leu Val Pro Gly Glu Pro Arg Cys Lys Thr Glu Ala Cys His			
50	55	60	
ccc ggc ccc atc cct caa ggt gaa acg tgc tgg gcc ctg ctc ctc cac			240
Pro Gly Pro Ile Pro Gln Gly Glu Thr Cys Trp Ala Leu Leu Leu His			
65	70	75	80
tgc tct gat cat caa gcc ttc atc cag ctc tgt gct ggg gcc acg gac			288
Cys Ser Asp His Gln Ala Phe Ile Gln Leu Cys Ala Gly Ala Thr Asp			
85	90	95	
agc gtg tct gga ggc acc att gac gtg gga cag cat cat ggg acc gca			336
Ser Val Ser Gly Gly Thr Ile Asp Val Gly Gln His His Gly Thr Ala			
100	105	110	
cat gca aga cat gcc cca aaa tgg tct cag aac cac act gct tct ggt			384
His Ala Arg His Ala Pro Lys Trp Ser Gln Asn His Thr Ala Ser Gly			
115	120	125	
gca gcc cac agc ggt ctt ttc cta taa			411
Ala Ala His Ser Gly Leu Phe Leu *			
130	135		

<210> 74

<211> 136

<212> PRT

<213> Homo sapiens

<400> 74

Met Arg Pro Leu Leu Leu Thr Lys Arg Ala Leu Leu Leu Pro Ser Ser			
1	5	10	15
His Leu Ala Gln Ala Glu Met Lys Leu Ala Phe Pro Met Phe Lys Val			
20	25	30	
Gln Ala Cys Gln Pro Asp Ser His Ser Ala Gln Arg Pro Leu Thr Gln			
35	40	45	

Leu Pro Leu Val Pro Gly Glu Pro Arg Cys Lys Thr Glu Ala Cys His
 50 55 60
 Pro Gly Pro Ile Pro Gln Gly Glu Thr Cys Trp Ala Leu Leu Leu His
 65 70 75 80
 Cys Ser Asp His Gln Ala Phe Ile Gln Leu Cys Ala Gly Ala Thr Asp
 85 90 95
 Ser Val Ser Gly Gly Thr Ile Asp Val Gly Gln His His Gly Thr Ala
 100 105 110
 His Ala Arg His Ala Pro Lys Trp Ser Gln Asn His Thr Ala Ser Gly
 115 120 125
 Ala Ala His Ser Gly Leu Phe Leu
 130 135

<210> 75
 <211> 678
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(678)

<400> 75

atg tac ttg gtg gcg ggg gac agg ggg ttg gcc ggc tgc ggg cac ctc	48
Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu	
1 5 10 15	
ctg gtc tcg ctg ctg ggg ctg ctg ctg ctg ctg gcg cgc tcc ggc acc	96
Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr	
20 25 30	
cgg gcg ctg gtc tgc ctg ccc tgt gac gag tcc aag tgc gag gag ccc	144
Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro	
35 40 45	
agg aac tgc ccg ggg agc atc gtg cag ggc gtc tgc ggc tgc tgc tac	192
Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr	
50 55 60	
acg tgc gcc agc cag agg aac gag agc tgc ggc ggc acc ttc ggg att	240
Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile	
65 70 75 80	

tac gga acc tgc gac cgg ggg ctg cgt tgt gtc atc cgc ccc ccg ctc	288
Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu	
85 90 95	
aat ggc gac tcc ctc acc gag tac gaa gcg ggc gtt tgc gaa ggt acg	336
Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Gly Thr	
100 105 110	
gcc gcc cgc tgc ggg ccc cct ccc acc tgg cct gcg ccg ccc cct cgg	384
Ala Ala Arg Cys Gly Pro Pro Thr Trp Pro Ala Pro Pro Pro Arg	
115 120 125	
cgc tgg ttg tgc cga aca aag ttt ggg cga gac ttt ctg gag gaa aga	432
Arg Trp Leu Cys Arg Thr Lys Phe Gly Arg Asp Phe Leu Glu Glu Arg	
130 135 140	
ggg ctc tgc ggg aag agg ggc ggc cgc cgc ccc cag gag agt gcc ccc	480
Gly Leu Cys Gly Lys Arg Gly Gly Arg Arg Pro Gln Glu Ser Ala Pro	
145 150 155 160	
gcg gcc ctg cgt tcc ctc tcc ttg ttc ccc ccg acg ctt agg cag tcg	528
Ala Ala Leu Arg Ser Leu Ser Leu Phe Pro Pro Thr Leu Arg Gln Ser	
165 170 175	
cgg gcg agg ttg ggt atg gct gcc tgc ctc cag gaa aat cac cta gaa	576
Arg Ala Arg Leu Gly Met Ala Ala Cys Leu Gln Glu Asn His Leu Glu	
180 185 190	
gcc aga gaa aca agt gtg gat cct gaa ccc ctg aga aag aaa tct gga	624
Ala Arg Glu Thr Ser Val Asp Pro Glu Pro Leu Arg Lys Lys Ser Gly	
195 200 205	
tgg aag aca tct ttg gag gat cga agg cag agt tta gaa aaa tta atg	672
Trp Lys Thr Ser Leu Glu Asp Arg Arg Gln Ser Leu Glu Lys Leu Met	
210 215 220	
aag tga	678
Lys *	
225	

<210> 76
<211> 225

<213> Homo sapiens

[illegible]

<211> 558

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(558)

<400> 77

atg gcc cgg gcc agg gcc ggg gcg ctg ctg gcg ctt tgg gtg ctc ggg	48
Met Ala Arg Ala Arg Ala Gly Ala Leu Leu Ala Leu Trp Val Leu Gly	
1 5 10 15	
gcc gcc gcg cat ccg cag tgc ctg gac ttc agg ccg ccc ttc cgg ccg	96
Ala Ala Ala His Pro Gln Cys Leu Asp Phe Arg Pro Pro Phe Arg Pro	
20 25 30	
acg cag ccg ctg cgc ctc tgc gcg cag tac tcg gac ttc ggc tgc tgc	144
Thr Gln Pro Leu Arg Leu Cys Ala Gln Tyr Ser Asp Phe Gly Cys Cys	
35 40 45	
gat gag ggg cgc gac gcc gag ctg acc cgc cgc ttc tgg gcc ctg gcg	192
Asp Glu Gly Arg Asp Ala Glu Leu Thr Arg Arg Phe Trp Ala Leu Ala	
50 55 60	
agc cgc gtg gac gcc gcc gag tgg gcc gcg tgc gcc ggc tac gcg agg	240
Ser Arg Val Asp Ala Ala Glu Trp Ala Ala Cys Ala Gly Tyr Ala Arg	
65 70 75 80	
gac ctg ctg tgc cag tcc gtg gag tgg aca gac atg caa aga gat aat	288
Asp Leu Leu Cys Gln Ser Val Glu Trp Thr Asp Met Gln Arg Asp Asn	
85 90 95	
gaa gtc cta gcc aag ctg act ggc tgg agc gcc cct ggc gac gga gca	336
Glu Val Leu Ala Lys Leu Thr Gly Trp Ser Ala Pro Gly Asp Gly Ala	
100 105 110	
gtg act gct gta gag aac tca ccc tgt aag cta caa gat tca atg gat	384
Val Thr Ala Val Glu Asn Ser Pro Cys Lys Leu Gln Asp Ser Met Asp	
115 120 125	
tct gga ttg ggc ttt ggt gaa cgg agg gct ctc gtt gcc ttc cag atg	432
Ser Gly Leu Gly Phe Gly Glu Arg Arg Ala Leu Val Ala Phe Gln Met	
130 135 140	
tct gtt ctg ccc ctc act gcg tct ctg gaa cca aga tgg tgc ctg gta	480
Ser Val Leu Pro Leu Thr Ala Ser Leu Glu Pro Arg Trp Cys Leu Val	
145 150 155 160	
caa tct ctg ctc agt aaa ttc ttg gtg aat gaa atg ttg ctg act aat	528

<221> CDS

<400> 79

atg	ccc	gcg	gcc	cgg	ccg	ccc	gcc	gcg	gga	ctc	cgc	ggg	atc	tcg	ctg	48
Met	Pro	Ala	Ala	Arg	Pro	Pro	Ala	Ala	Gly	Leu	Arg	Gly	Ile	Ser	Leu	
1				5					10					15		
ttc	ctc	gct	ctg	ctc	ctg	ggg	agc	ccg	gcg	gca	gcg	ctg	gag	cga	ggg	96
Phe	Leu	Ala	Leu	Leu	Leu	Gly	Ser	Pro	Ala	Ala	Ala	Leu	Glu	Arg	Gly	
			20					25					30			
gtg	gtc	agt	gaa	ggc	ttc	ctg	gag	cac	gta	gca	ttt	gaa	ctg	gcc	ctg	144
Val	Val	Ser	Glu	Gly	Phe	Leu	Glu	His	Val	Ala	Phe	Glu	Leu	Ala	Leu	
		35					40					45				
aag	ggg	ata	gga	cag	aca	cag	acc	ctg	gag	tcc	aag	aga	tat	ggg	ttc	192
Lys	Gly	Ile	Gly	Gln	Thr	Gln	Thr	Leu	Glu	Ser	Lys	Arg	Tyr	Gly	Phe	
	50					55					60					
aaa	cct	aat	gct	gtg	atc	ttg	aac	aag	tca	ctt	aac	tct	gag	atg	atg	240
Lys	Pro	Asn	Ala	Val	Ile	Leu	Asn	Lys	Ser	Leu	Asn	Ser	Glu	Met	Met	
65					70				75					80		
gga	gtg	ggt	ggt	agt	gat	gag	gat	gaa	gag	ggg	aat	tat	gag	ttg	ctg	288
Gly	Val	Gly	Gly	Ser	Asp	Glu	Asp	Glu	Glu	Gly	Asn	Tyr	Glu	Leu	Leu	
				85				90						95		
ttg	tta	ctg	atg	gac	cga	gct	gat	tct	cag	aca	ttt	aaa	agt	gat	cca	336
Leu	Leu	Leu	Met	Asp	Arg	Ala	Asp	Ser	Gln	Thr	Phe	Lys	Ser	Asp	Pro	
			100					105					110			
ggc	att	gaa	aat	cag	gtt	gga	gtg	gaa	aat	gaa	gag	aag	cct	caa	ggt	384
Gly	Ile	Glu	Asn	Gln	Val	Gly	Val	Glu	Asn	Glu	Glu	Lys	Pro	Gln	Gly	
		115					120					125				
ggg	gtc	cca	gga	gct	ctc	ccc	ttt	tcc	cat	gag	aga	ttc	atc	tgg	aat	432
Gly	Val	Pro	Gly	Ala	Leu	Pro	Phe	Ser	His	Glu	Arg	Phe	Ile	Trp	Asn	
	130					135					140					
gat	gac	agt	gga	ttt	aag	agc	aat	aag	gga	ggg	gaa	cgg	ctg	agc	cag	480

Asp Asp Ser Gly Phe Lys Ser Asn Lys Gly Gly Glu Arg Leu Ser Gln
 145 150 155 160

 gga cct gtg gac act cag gat tca act ctg ggc ttg gcc aga gat aag 528
 Gly Pro Val Asp Thr Gln Asp Ser Thr Leu Gly Leu Ala Arg Asp Lys
 165 170 175

 tcc tta gag ttt ggg gca ttt gaa caa ctg aca aga agc cag cat ggc 576
 Ser Leu Glu Phe Gly Ala Phe Glu Gln Leu Thr Arg Ser Gln His Gly
 180 185 190

 cag aat atc ctg aac aga gaa gga agt ggg caa atg aag tta aga gaa 624
 Gln Asn Ile Leu Asn Arg Glu Gly Ser Gly Gln Met Lys Leu Arg Glu
 195 200 205

 agt att aaa gaa aag caa tga 645
 Ser Ile Lys Glu Lys Gln *
 210

<210> 80
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 80

Met Pro Ala Ala Arg Pro Pro Ala Ala Gly Leu Arg Gly Ile Ser Leu
 1 5 10 15
 Phe Leu Ala Leu Leu Gly Ser Pro Ala Ala Ala Leu Glu Arg Gly
 20 25 30
 Val Val Ser Glu Gly Phe Leu Glu His Val Ala Phe Glu Leu Ala Leu
 35 40 45
 Lys Gly Ile Gly Gln Thr Gln Thr Leu Glu Ser Lys Arg Tyr Gly Phe
 50 55 60
 Lys Pro Asn Ala Val Ile Leu Asn Lys Ser Leu Asn Ser Glu Met Met
 65 70 75 80
 Gly Val Gly Gly Ser Asp Glu Asp Glu Glu Gly Asn Tyr Glu Leu Leu
 85 90 95
 Leu Leu Leu Met Asp Arg Ala Asp Ser Gln Thr Phe Lys Ser Asp Pro
 100 105 110
 Gly Ile Glu Asn Gln Val Gly Val Glu Asn Glu Glu Lys Pro Gln Gly
 115 120 125
 Gly Val Pro Gly Ala Leu Pro Phe Ser His Glu Arg Phe Ile Trp Asn

130 135 140
 Asp Asp Ser Gly Phe Lys Ser Asn Lys Gly Gly Glu Arg Leu Ser Gln
 145 150 155 160
 Gly Pro Val Asp Thr Gln Asp Ser Thr Leu Gly Leu Ala Arg Asp Lys
 165 170 175
 Ser Leu Glu Phe Gly Ala Phe Glu Gln Leu Thr Arg Ser Gln His Gly
 180 185 190
 Gln Asn Ile Leu Asn Arg Glu Gly Ser Gly Gln Met Lys Leu Arg Glu
 195 200 205
 Ser Ile Lys Glu Lys Gln
 210

<210> 81
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(303)

<400> 81
 atg gca gcc ttg ctg ctc ttg acc ctc agc ctg att cag gtc tca ggg 48
 Met Ala Ala Leu Leu Leu Leu Thr Leu Ser Leu Ile Gln Val Ser Gly
 1 5 10 15
 gtg ctg ctg acc tcc agt gtg gac agt ccc tct acc ctg ccg ctg tct 96
 Val Leu Leu Thr Ser Ser Val Asp Ser Pro Ser Thr Leu Pro Leu Ser
 20 25 30
 gca cag aga acc gtc cac cgt ggc ctc ttt aca ttc caa gct gga ttt 144
 Ala Gln Arg Thr Val His Arg Gly Leu Phe Thr Phe Gln Ala Gly Phe
 35 40 45
 tct cct gat cgc tcc agt tct cga ggc aaa aag caa aga gtc tcg ggc 192
 Ser Pro Asp Arg Ser Ser Ser Arg Gly Lys Lys Gln Arg Val Ser Gly
 50 55 60
 tgc aat gac atg gtt tgc ttc ggg ttc tcc ggc gcc gcc tgc ctc ctc 240
 Cys Asn Asp Met Val Cys Phe Gly Phe Ser Gly Ala Ala Cys Leu Leu
 65 70 75 80
 tgt cag atg ccg gtg ttc ggg ggc ggc ttc gtt ggc ttc ctt cct tct 288

48

gtg gtc ggt gcc tcc acg cca ggc acc gtg gtc cga ctc aac aag gca Val Val Gly Ala Ser Thr Pro Gly Thr Val Val Arg Leu Asn Lys Ala 20 25 30	96
gca ttg agc tac gtg tct gaa att ggg aaa gcc cct ctc cag cgg gcc Ala Leu Ser Tyr Val Ser Glu Ile Gly Lys Ala Pro Leu Gln Arg Ala 35 40 45	144
ctg cag gtc act gtc cct cat ttc ctg gac tgg agt gga gag gcg ctt Leu Gln Val Thr Val Pro His Phe Leu Asp Trp Ser Gly Glu Ala Leu 50 55 60	192
cag ccc acc agg atc cgg att ctg aat gtc cat gtg ccc cgc ctc cac Gln Pro Thr Arg Ile Arg Ile Leu Asn Val His Val Pro Arg Leu His 65 70 75 80	240
ctg aaa ttc att gct ggt ttc gga gtg cgc ctg ctg gca gca gct aat Leu Lys Phe Ile Ala Gly Phe Gly Val Arg Leu Leu Ala Ala Ala Asn 85 90 95	288
ttt act ttc aag gtc ttt cgc gcc cca gag ccc ctg gag ctg acg ctg Phe Thr Phe Lys Val Phe Arg Ala Pro Glu Pro Leu Glu Leu Thr Leu 100 105 110	336
cct gtg gaa ctg ctg gct gac acc cgc gtg acc cag agc tcc atc agg Pro Val Glu Leu Leu Ala Asp Thr Arg Val Thr Gln Ser Ser Ile Arg 115 120 125	384
acc cct gtg gtc agc atc tct gcc tgc tct tta ttc tcg ggc cac gcc Thr Pro Val Val Ser Ile Ser Ala Cys Ser Leu Phe Ser Gly His Ala 130 135 140	432
aac gag ttt gat ggc agt aac agc acc tcc cac gcg ctg ctg gtc ctg Asn Glu Phe Asp Gly Ser Asn Ser Thr Ser His Ala Leu Leu Val Leu 145 150 155 160	480
gtg cag aag cac att aaa gct gtc ttg agt aac aag ctg tgc ctg agc Val Gln Lys His Ile Lys Ala Val Leu Ser Asn Lys Leu Cys Leu Ser 165 170 175	528
atc tcc aac ctg gtg cag ggt gtc aat gtc cac ctg ggc acc tta att Ile Ser Asn Leu Val Gln Gly Val Asn Val His Leu Gly Thr Leu Ile 180 185 190	576

ggc ctc aac ccc gtg ggt cct gag tcc cag atc cgc tat tcc atg gtc Gly Leu Asn Pro Val Gly Pro Glu Ser Gln Ile Arg Tyr Ser Met Val 195 200 205	624
agt gtg ccc act gtc acc agt gac tac att tcc ctg gaa gtc aat gct Ser Val Pro Thr Val Thr Ser Asp Tyr Ile Ser Leu Glu Val Asn Ala 210 215 220	672
gtt ctc ttc ctg ctg ggc aag ccc atc atc ctg ccc acg gat gcc acc Val Leu Phe Leu Leu Gly Lys Pro Ile Ile Leu Pro Thr Asp Ala Thr 225 230 235 240	720
cct ttt gtg ttg cca agg cat gtg ggt acc gag ggc tcc atg gcc acc Pro Phe Val Leu Pro Arg His Val Gly Thr Glu Gly Ser Met Ala Thr 245 250 255	768
gtg ggc ctc tcc cag cag ctg ttt gac tct gcg ctc ctg ctg ctg cag Val Gly Leu Ser Gln Gln Leu Phe Asp Ser Ala Leu Leu Leu Leu Gln 260 265 270	816
aag gcc ggt gcc ctc aac ctg gac atc aca ggg cag ctg gtg gcc cgc Lys Ala Gly Ala Leu Asn Leu Asp Ile Thr Gly Gln Leu Val Ala Arg 275 280 285	864
cag ttt ccc gag ccc atg cct gtg gtg ctc aag gtg cgg ctg ggt gcc Gln Phe Pro Glu Pro Met Pro Val Val Leu Lys Val Arg Leu Gly Ala 290 295 300	912
aca cct gtg gcc atg ctc cac aca aac aac gcc acc ctg cgg ctg cag Thr Pro Val Ala Met Leu His Thr Asn Asn Ala Thr Leu Arg Leu Gln 305 310 315 320	960
ccc ttc gtg gag gtc ctg gcc aca gcc tcc aac tcg gct ttc cag tcc Pro Phe Val Glu Val Leu Ala Thr Ala Ser Asn Ser Ala Phe Gln Ser 325 330 335	1008
ctc ttc tcc ctg gat gtg gta gtg aac ttg aga ctc cag ctc tct gtg Leu Phe Ser Leu Asp Val Val Val Asn Leu Arg Leu Gln Leu Ser Val 340 345 350	1056
tcc aag gtg aag ctt cag ggg acc acg tct gtg ctg ggg gat gtc cag Ser Lys Val Lys Leu Gln Gly Thr Thr Ser Val Leu Gly Asp Val Gln	1104

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<210> 84
<211> 510
<212> PRT
<213> Homo sapiens
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<400> 84

Met Ala Trp Ala Ser Arg Leu Gly Leu Leu Leu Ala Leu Leu Leu Pro
 1 5 10 15
 Val Val Gly Ala Ser Thr Pro Gly Thr Val Val Arg Leu Asn Lys Ala
 20 25 30
 Ala Leu Ser Tyr Val Ser Glu Ile Gly Lys Ala Pro Leu Gln Arg Ala
 35 40 45
 Leu Gln Val Thr Val Pro His Phe Leu Asp Trp Ser Gly Glu Ala Leu
 50 55 60
 Gln Pro Thr Arg Ile Arg Ile Leu Asn Val His Val Pro Arg Leu His
 65 70 75 80
 Leu Lys Phe Ile Ala Gly Phe Gly Val Arg Leu Leu Ala Ala Ala Asn
 85 90 95
 Phe Thr Phe Lys Val Phe Arg Ala Pro Glu Pro Leu Glu Leu Thr Leu
 100 105 110
 Pro Val Glu Leu Leu Ala Asp Thr Arg Val Thr Gln Ser Ser Ile Arg
 115 120 125
 Thr Pro Val Val Ser Ile Ser Ala Cys Ser Leu Phe Ser Gly His Ala
 130 135 140
 Asn Glu Phe Asp Gly Ser Asn Ser Thr Ser His Ala Leu Leu Val Leu
 145 150 155 160
 Val Gln Lys His Ile Lys Ala Val Leu Ser Asn Lys Leu Cys Leu Ser
 165 170 175
 Ile Ser Asn Leu Val Gln Gly Val Asn Val His Leu Gly Thr Leu Ile
 180 185 190
 Gly Leu Asn Pro Val Gly Pro Glu Ser Gln Ile Arg Tyr Ser Met Val
 195 200 205
 Ser Val Pro Thr Val Thr Ser Asp Tyr Ile Ser Leu Glu Val Asn Ala
 210 215 220
 Val Leu Phe Leu Leu Gly Lys Pro Ile Ile Leu Pro Thr Asp Ala Thr
 225 230 235 240
 Pro Phe Val Leu Pro Arg His Val Gly Thr Glu Gly Ser Met Ala Thr
 245 250 255
 Val Gly Leu Ser Gln Gln Leu Phe Asp Ser Ala Leu Leu Leu Leu Gln
 260 265 270
 Lys Ala Gly Ala Leu Asn Leu Asp Ile Thr Gly Gln Leu Val Ala Arg
 275 280 285
 Gln Phe Pro Glu Pro Met Pro Val Val Leu Lys Val Arg Leu Gly Ala
 290 295 300
 Thr Pro Val Ala Met Leu His Thr Asn Asn Ala Thr Leu Arg Leu Gln
 305 310 315 320
 Pro Phe Val Glu Val Leu Ala Thr Ala Ser Asn Ser Ala Phe Gln Ser

Leu Pro Ala His Ser Asn Glu Arg Lys Leu Arg Gly Ser Pro Gln Val
 35 40 45

 cca gcc aag tct tca gag ccg gcc act ctg gcc aac agc ttg agt aca 192
 Pro Ala Lys Ser Ser Glu Pro Ala Thr Leu Ala Asn Ser Leu Ser Thr
 50 55 60

 act gca cgc aag ccg caa gcc gga acc act ggg cta gga tgc tcc cag 240
 Thr Ala Arg Lys Pro Gln Ala Gly Thr Thr Gly Leu Gly Cys Ser Gln
 65 70 75 80

 att ctg agc tct gag gat ttg act cag gca aag att att gct gct ggc 288
 Ile Leu Ser Ser Glu Asp Leu Thr Gln Ala Lys Ile Ile Ala Ala Gly
 85 90 95

 aga agg tcg agg caa aaa ttc tct acc ttg gag gga agg gtg gat aca 336
 Arg Arg Ser Arg Gln Lys Phe Ser Thr Leu Glu Gly Arg Val Asp Thr
 100 105 110

 gat atc aaa cag atg tct agt ctt gct agg aat ggg gcc gaa aac tcc 384
 Asp Ile Lys Gln Met Ser Ser Leu Ala Arg Asn Gly Ala Glu Asn Ser
 115 120 125

 cac cct acg cca acc atg gac aca agg aga agt ttg gca gcc aca ggt 432
 His Pro Thr Pro Thr Met Asp Thr Arg Arg Ser Leu Ala Ala Thr Gly
 130 135 140

 aga agg agc aag aat gct tag 453
 Arg Arg Ser Lys Asn Ala *
 145 150

<210> 86

<211> 150

<212> PRT

<213> Homo sapiens

<400> 86

Met Ala Val Leu Val Val Ser Leu Gly Ser Leu Ala Leu Gly Glu Glu
 1 5 10 15
 Val Leu Leu Val Ala Pro Trp Arg Gly Pro His Ser Lys Glu Leu Lys
 20 25 30
 Leu Pro Ala His Ser Asn Glu Arg Lys Leu Arg Gly Ser Pro Gln Val

```
<210> 87
<211> 438
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(438)
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<400> 87																
atg	ggc	cgc	cgc	cgc	ctg	ctc	gtc	tgg	ctg	tgc	gcc	gtc	gcg	gcg	ctg	48
Met	Gly	Arg	Arg	Arg	Leu	Leu	Val	Trp	Leu	Cys	Ala	Val	Ala	Ala	Leu	
1		5			10				15							
ctc	tcg	ggg	gcg	cag	gcc	agg	ggc	acc	ccg	ctc	ctg	gcg	cgg	cct	gcg	96
Leu	Ser	Gly	Ala	Gln	Ala	Arg	Gly	Thr	Pro	Leu	Leu	Ala	Arg	Pro	Ala	
20				25				30								
ccg	ccc	ggt	gcc	tcc	cgc	tac	agt	ctc	tac	acg	acg	gga	tgg	cgc	ccg	144
Pro	Pro	Gly	Ala	Ser	Arg	Tyr	Ser	Leu	Tyr	Thr	Thr	Gly	Trp	Arg	Pro	
35			40				45									
cgg	ctg	cgc	ccg	ggg	ccg	cac	aag	gcc	ctc	tgt	gcc	tat	gtg	gtg	cac	192
Arg	Leu	Arg	Pro	Gly	Pro	His	Lys	Ala	Leu	Cys	Ala	Tyr	Val	Val	His	
50			55				60									
agg	aat	gtg	acc	tgc	atc	cta	cag	gag	gga	gcg	gag	agc	tac	gta	aag	240

Arg Asn Val Thr Cys Ile Leu Gln Glu Gly Ala Glu Ser Tyr Val Lys
 65 70 75 80
 gct gaa tac cgg cag tgt aga tgg ggg ccc aag tgc ccc ggg aca gtc 288
 Ala Glu Tyr Arg Gln Cys Arg Trp Gly Pro Lys Cys Pro Gly Thr Val
 85 90 95
 acg cca cag acc gcg tat gcg ttc aga ctc cag gag cgt ctc tcg agt 336
 Thr Pro Gln Thr Ala Tyr Ala Phe Arg Leu Gln Glu Arg Leu Ser Ser
 100 105 110
 ggg tct gca tct cat gca gaa tat cgc ggg tct cac gac agc att aat 384
 Gly Ser Ala Ser His Ala Glu Tyr Arg Gly Ser His Asp Ser Ile Asn
 115 120 125
 cga gga ctc ggt tca cta cgg tgt gct cgg atg tat gct cag cta gtt 432
 Arg Gly Leu Gly Ser Leu Arg Cys Ala Arg Met Tyr Ala Gln Leu Val
 130 135 140
 att tga 438
 Ile *
 145

<210> 88
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Gly Arg Arg Arg Leu Leu Val Trp Leu Cys Ala Val Ala Ala Leu
 1 5 10 15
 Leu Ser Gly Ala Gln Ala Arg Gly Thr Pro Leu Leu Ala Arg Pro Ala
 20 25 30
 Pro Pro Gly Ala Ser Arg Tyr Ser Leu Tyr Thr Thr Gly Trp Arg Pro
 35 40 45
 Arg Leu Arg Pro Gly Pro His Lys Ala Leu Cys Ala Tyr Val Val His
 50 55 60
 Arg Asn Val Thr Cys Ile Leu Gln Glu Gly Ala Glu Ser Tyr Val Lys
 65 70 75 80
 Ala Glu Tyr Arg Gln Cys Arg Trp Gly Pro Lys Cys Pro Gly Thr Val
 85 90 95
 Thr Pro Gln Thr Ala Tyr Ala Phe Arg Leu Gln Glu Arg Leu Ser Ser

```
<210> 89
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(372)
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<400> 89																
atg	ctg	ctg	ctg	ctc	ctg	ttg	ctg	ctg	ctg	cta	cag	ctc	cag	gcc	ctt	48
Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Gln	Ala	Leu	
1		5			10					15						
gct	ctg	gtg	cca	ctg	gag	caa	aat	ctc	tcc	cca	aga	ccc	cgg	gtg	aag	96
Ala	Leu	Val	Pro	Leu	Glu	Gln	Asn	Leu	Ser	Pro	Arg	Pro	Arg	Val	Lys	
20			25					30								
agt	gct	gct	cca	aca	caa	caa	cca	gtc	acc	tgc	ttg	ctg	agg	att	ggt	144
Ser	Ala	Ala	Pro	Thr	Gln	Gln	Pro	Val	Thr	Cys	Leu	Leu	Arg	Ile	Gly	
35			40					45								
tgt	cat	gct	cct	gct	tgg	ccc	aca	agc	atc	tcc	cac	aag	aaa	ttc	tgc	192
Cys	His	Ala	Pro	Ala	Trp	Pro	Thr	Ser	Ile	Ser	His	Lys	Lys	Phe	Cys	
50		55					60									
agg	aaa	tcc	agg	gtc	ctg	tct	gaa	ccc	aaa	gat	ggt	tct	atc	tat	cga	240
Arg	Lys	Ser	Arg	Val	Leu	Ser	Glu	Pro	Lys	Asp	Val	Ser	Ile	Tyr	Arg	
65		70					75							80		
atg	ttc	cct	ggt	cat	tgg	ttg	aag	gcc	atc	aag	tgc	gcg	gtg	aaa	gtc	288
Met	Phe	Pro	Gly	His	Trp	Leu	Lys	Ala	Ile	Lys	Ser	Ala	Val	Lys	Val	
85				90						95						
tta	ccc	agt	act	tac	aca	gta	ctt	cag	ctt	agc	tgc	gaa	aat	atc	aat	336

gag ctg ccg aac tgt gtg gac ccc aag cca ggc tga
Glu Leu Pro Asn Cys Val Asp Pro Lys Pro Gly *

```
<210> 90
<211> 123
<212> PRT
<213> Homo sapiens
```

<400> 90															
Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Gln	Ala	Leu
1				5					10					15	
Ala	Leu	Val	Pro	Leu	Glu	Gln	Asn	Leu	Ser	Pro	Arg	Pro	Arg	Val	Lys
			20					25					30		
Ser	Ala	Ala	Pro	Thr	Gln	Gln	Pro	Val	Thr	Cys	Leu	Leu	Arg	Ile	Gly
		35					40					45			
Cys	His	Ala	Pro	Ala	Trp	Pro	Thr	Ser	Ile	Ser	His	Lys	Lys	Phe	Cys
	50					55					60				
Arg	Lys	Ser	Arg	Val	Leu	Ser	Glu	Pro	Lys	Asp	Val	Ser	Ile	Tyr	Arg
65					70					75					80
Met	Phe	Pro	Gly	His	Trp	Leu	Lys	Ala	Ile	Lys	Ser	Ala	Val	Lys	Val
				85					90					95	
Leu	Pro	Ser	Thr	Tyr	Thr	Val	Leu	Gln	Leu	Ser	Cys	Glu	Asn	Ile	Asn
			100					105					110		
Glu	Leu	Pro	Asn	Cys	Val	Asp	Pro	Lys	Pro	Gly					
		115						120							

```
<210> 91
<211> 618
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (1)...(618)

<400> 91
atg gag ttg ctg tta ctg gcg gtg ttg agt cgg ggg act ggg gca gtt
Met Glu Leu Leu Leu Leu Ala Val Leu Ser Arg Gly Thr Gly Ala Val

1	5	10	15	
gca ctg ctg tct gac tgc att ttc aaa ggg cag cag tgc tgt gct ggg				96
Ala Leu Leu Ser Asp Cys Ile Phe Lys Gly Gln Gln Cys Cys Ala Gly				
20	25	30		
ggc ctg ctc cag tcc cta gtc acc tcg tac tcc cta aat gct gaa ggc				144
Gly Leu Leu Gln Ser Leu Val Thr Ser Tyr Ser Leu Asn Ala Glu Gly				
35	40	45		
aaa caa cag cta agg ctg caa aac agc aaa gat gat gac ctg ccc ctc				192
Lys Gln Gln Leu Arg Leu Gln Asn Ser Lys Asp Asp Asp Leu Pro Leu				
50	55	60		
cct ctg gga gct cca acc cac ggg ggg atg ggg ctg ctg aaa aca cca				240
Pro Leu Gly Ala Pro Thr His Gly Gly Met Gly Leu Leu Lys Thr Pro				
65	70	75	80	
gca aag ggt gac tgg aga ccc tgg tcc tgc cca aat tcg gct gtg aat				288
Ala Lys Gly Asp Trp Arg Pro Trp Ser Cys Pro Asn Ser Ala Val Asn				
85	90	95		
cca tct ggt cct gga ctc ttt ttg gtt ggt aaa cta ttg att att gcc				336
Pro Ser Gly Pro Gly Leu Phe Leu Val Gly Lys Leu Leu Ile Ile Ala				
100	105	110		
aca att tca gag cct gtt att ggt cta ttc aga gat tca act tct tcc				384
Thr Ile Ser Glu Pro Val Ile Gly Leu Phe Arg Asp Ser Thr Ser Ser				
115	120	125		
tgg ttt agt ctt ggg aga gtg tat gtg tcg agg aat gta tcc att tct				432
Trp Phe Ser Leu Gly Arg Val Tyr Val Ser Arg Asn Val Ser Ile Ser				
130	135	140		
tac aac gga tgt gaa gga cct ctt caa gga gaa cta caa acc act gct				480
Tyr Asn Gly Cys Glu Gly Pro Leu Gln Gly Glu Leu Gln Thr Thr Ala				
145	150	155	160	
caa gga aat aaa aga gga cac aaa caa atg gaa gaa cat tcc atg ctc				528
Gln Gly Asn Lys Arg Gly His Lys Gln Met Glu Glu His Ser Met Leu				
165	170	175		
atg ggt agg aag aat caa tat cgt gaa aat ggc cat act gcc caa gac				576

Met Gly Arg Lys Asn Gln Tyr Arg Glu Asn Gly His Thr Ala Gln Asp
 180 185 190

ctc cag gac tgt gat gag agg ggc tac tgc caa gat ctc tga
 Leu Gln Asp Cys Asp Glu Arg Gly Tyr Cys Gln Asp Leu *
 195 200 205

618

<210> 92

<211> 205

<212> PRT

<213> Homo sapiens

<400> 92

Met Glu Leu Leu Leu Leu Ala Val Leu Ser Arg Gly Thr Gly Ala Val
 1 5 10 15
 Ala Leu Leu Ser Asp Cys Ile Phe Lys Gly Gln Gln Cys Cys Ala Gly
 20 25 30
 Gly Leu Leu Gln Ser Leu Val Thr Ser Tyr Ser Leu Asn Ala Glu Gly
 35 40 45
 Lys Gln Gln Leu Arg Leu Gln Asn Ser Lys Asp Asp Asp Leu Pro Leu
 50 55 60
 Pro Leu Gly Ala Pro Thr His Gly Gly Met Gly Leu Leu Lys Thr Pro
 65 70 75 80
 Ala Lys Gly Asp Trp Arg Pro Trp Ser Cys Pro Asn Ser Ala Val Asn
 85 90 95
 Pro Ser Gly Pro Gly Leu Phe Leu Val Gly Lys Leu Leu Ile Ile Ala
 100 105 110
 Thr Ile Ser Glu Pro Val Ile Gly Leu Phe Arg Asp Ser Thr Ser Ser
 115 120 125
 Trp Phe Ser Leu Gly Arg Val Tyr Val Ser Arg Asn Val Ser Ile Ser
 130 135 140
 Tyr Asn Gly Cys Glu Gly Pro Leu Gln Gly Glu Leu Gln Thr Thr Ala
 145 150 155 160
 Gln Gly Asn Lys Arg Gly His Lys Gln Met Glu Glu His Ser Met Leu
 165 170 175
 Met Gly Arg Lys Asn Gln Tyr Arg Glu Asn Gly His Thr Ala Gln Asp
 180 185 190
 Leu Gln Asp Cys Asp Glu Arg Gly Tyr Cys Gln Asp Leu
 195 200 205

<210> 93

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(342)

<400> 93

atg gcg gcg gcc cca cgc gcg ggc cgg cgg cgc ggg cag ccg ctc ctg	48
Met Ala Ala Ala Pro Arg Ala Gly Arg Arg Arg Gly Gln Pro Leu Leu	
1 5 10 15	
gcg ctg ctg ctt ctg ctg ctg gcg cca ctg ccg ccg ggg gcc ccg ccg	96
Ala Leu Leu Leu Leu Leu Leu Ala Pro Leu Pro Pro Gly Ala Pro Pro	
20 25 30	
ggc gcc gac gcc tac ttc ccc gag gag cgc tgg agc ccg gag tcg ccc	144
Gly Ala Asp Ala Tyr Phe Pro Glu Glu Arg Trp Ser Pro Glu Ser Pro	
35 40 45	
ctg cag gcg ccg cgc gtg ctc atc gcg ctg ttg gcg cga aac gcg gcc	192
Leu Gln Ala Pro Arg Val Leu Ile Ala Leu Leu Ala Arg Asn Ala Ala	
50 55 60	
cac gcg ttg ccc acc acg ctg ggc gca ctc gag cgg ctg cgg cac ccg	240
His Ala Leu Pro Thr Thr Leu Gly Ala Leu Glu Arg Leu Arg His Pro	
65 70 75 80	
cgg gag cgc acg gcg cta tgg acg gag ccc aga gcc ccc act ggg gcg	288
Arg Glu Arg Thr Ala Leu Trp Thr Glu Pro Arg Ala Pro Thr Gly Ala	
85 90 95	
ttg cca gag gcc aca tct aac agc aag cct ttc tgt gcc ggc tgc tgc	336
Leu Pro Glu Ala Thr Ser Asn Ser Lys Pro Phe Cys Ala Gly Cys Cys	
100 105 110	
cct taa	342
Pro *	

<210> 94

<211> 113

<213> Homo sapiens

[illegible]

<211> 343

$\langle 213 \rangle$ Hom

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (343)$

atg	aca	gca	agc	cgc	cag	atg	ttt	aga	ctt	tct	gtt	ctc	ctt	gct	ggc	48
Met	Thr	Ala	Ser	Arg	Gln	Met	Phe	Arg	Leu	Ser	Val	Leu	Leu	Ala	Gly	
1				5					10					15		
tct	gta	ttg	cca	gcc	ctg	gct	act	gct	gtt	aga	aac	ctt	tct	gag	act	96
Ser	Val	Leu	Pro	Ala	Leu	Ala	Thr	Ala	Val	Arg	Asn	Leu	Ser	Glu	Thr	
			20					25					30			
aga	cca	gtt	aaa	ctt	gtg	gtt	ccg	tgg	gtt	gat	atc	cag	aaa	tta	gaa	144
Arg	Pro	Val	Lys	Leu	Val	Val	Pro	Trp	Val	Asp	Ile	Gln	Lys	Leu	Glu	
		35					40					45				

[illegible]

<210> 97
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(420)

<400> 97

atg ctg ctg ctg ctg ctg ttg ttt atg aga cag ggt ctg gct ctg tca	48
Met Leu Leu Leu Leu Leu Leu Phe Met Arg Gln Gly Leu Ala Leu Ser	
1 5 10 15	
ccc agc ctg gag tgc agt gac gtc atc att gcc cac tgc agc ctc agc	96
Pro Ser Leu Glu Cys Ser Asp Val Ile Ile Ala His Cys Ser Leu Ser	
20 25 30	
ctc gtg ggc tcg agt gat cct cct gaa aca aca tat att ggc acc ctc	144
Leu Val Gly Ser Ser Asp Pro Pro Glu Thr Thr Tyr Ile Gly Thr Leu	
35 40 45	
ctt gtg tct gtg aat cca tac cag gag ctc gga atc tac act gtg ctg	192
Leu Val Ser Val Asn Pro Tyr Gln Glu Leu Gly Ile Tyr Thr Val Leu	
50 55 60	
tgc aag tcc aag aac att atc ctg agg gaa tgc ttc ctg ctg gcc gag	240
Cys Lys Ser Lys Asn Ile Ile Leu Arg Glu Cys Phe Leu Leu Ala Glu	
65 70 75 80	
tta gaa aac cgg agg agg ccc cca aca ggc ttg tcc aat aag ggt gtg	288
Leu Glu Asn Arg Arg Arg Pro Pro Thr Gly Leu Ser Asn Lys Gly Val	
85 90 95	
gcc tat ctc cct act gga cct ctt ctg gag gga gcc tca acg ccc aaa	336
Ala Tyr Leu Pro Thr Gly Pro Leu Leu Glu Gly Ala Ser Thr Pro Lys	
100 105 110	
aga cct aat aac aac aat aaa att gtg ggc aca ttg cca atg atg gga	384
Arg Pro Asn Asn Asn Asn Lys Ile Val Gly Thr Leu Pro Met Met Gly	
115 120 125	

ggt ggc tcc ccc aag gct caa gag tgg agc tgg tga
 Gly Gly Ser Pro Lys Ala Gln Glu Trp Ser Trp *
 130 135

420

<210> 98
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 98

Met Leu Leu Leu Leu Leu Leu Phe Met Arg Gln Gly Leu Ala Leu Ser
 1 5 10 15
 Pro Ser Leu Glu Cys Ser Asp Val Ile Ile Ala His Cys Ser Leu Ser
 20 25 30
 Leu Val Gly Ser Ser Asp Pro Pro Glu Thr Thr Tyr Ile Gly Thr Leu
 35 40 45
 Leu Val Ser Val Asn Pro Tyr Gln Glu Leu Gly Ile Tyr Thr Val Leu
 50 55 60
 Cys Lys Ser Lys Asn Ile Ile Leu Arg Glu Cys Phe Leu Leu Ala Glu
 65 70 75 80
 Leu Glu Asn Arg Arg Arg Pro Pro Thr Gly Leu Ser Asn Lys Gly Val
 85 90 95
 Ala Tyr Leu Pro Thr Gly Pro Leu Leu Glu Gly Ala Ser Thr Pro Lys
 100 105 110
 Arg Pro Asn Asn Asn Asn Lys Ile Val Gly Thr Leu Pro Met Met Gly
 115 120 125
 Gly Gly Ser Pro Lys Ala Gln Glu Trp Ser Trp
 130 135

<210> 99
 <211> 2172
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2172)

<400> 99

atg gct ctc agc ctc tgg ccc ctg ctg ctg ctg ctg ctg ctg ctg
 Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu
 1 5 10 15

48

ctg ctg tcc ttt gca gtg act ctg gcc cct act ggg cct cat tcc ctg	96
Leu Leu Ser Phe Ala Val Thr Leu Ala Pro Thr Gly Pro His Ser Leu	
20 25 30	
gac cct ggt ctc tcc ttc ctg aag tca ttg ctc tcc act ctg gac cag	144
Asp Pro Gly Leu Ser Phe Leu Lys Ser Leu Leu Ser Thr Leu Asp Gln	
35 40 45	
gct ccc cag ggc tcc ctg agc cgc tca cgg ttc ttt aca ttc ctg gcc	192
Ala Pro Gln Gly Ser Leu Ser Arg Ser Arg Phe Phe Thr Phe Leu Ala	
50 55 60	
aac att tct tct tcc ttt gag cct ggg aga atg ggg gaa gga cca gta	240
Asn Ile Ser Ser Ser Phe Glu Pro Gly Arg Met Gly Glu Gly Pro Val	
65 70 75 80	
gga gag ccc cca cct ctc cag ccg cct gct ctg cgg ctc cat gat ttt	288
Gly Glu Pro Pro Pro Leu Gln Pro Pro Ala Leu Arg Leu His Asp Phe	
85 90 95	
cta gtg aca ctg aga ggt agc ccc gac tgg gag cca atg cta ggg ctg	336
Leu Val Thr Leu Arg Gly Ser Pro Asp Trp Glu Pro Met Leu Gly Leu	
100 105 110	
cta ggg gat atg ctg gca ctg ctg gga cag gag cag act ccc cga gat	384
Leu Gly Asp Met Leu Ala Leu Leu Gly Gln Glu Gln Thr Pro Arg Asp	
115 120 125	
ttc ctg gtg cac cag gca ggg gtg ctg ggt gga ctt gtg gag gtg ctg	432
Phe Leu Val His Gln Ala Gly Val Leu Gly Gly Leu Val Glu Val Leu	
130 135 140	
ctg gga gcc tta gtt cct ggg ggc ccc cct acc cca act cgg ccc cca	480
Leu Gly Ala Leu Val Pro Gly Gly Pro Pro Thr Pro Thr Arg Pro Pro	
145 150 155 160	
tgc acc cgt gat ggg ccg tct gac tgt gtc ctg gct gct gac tgg ttg	528
Cys Thr Arg Asp Gly Pro Ser Asp Cys Val Leu Ala Ala Asp Trp Leu	
165 170 175	
cct tct ctg ctg ctg ttg tta gag ggc aca cgc tgg caa gct ctg gtg	576
Pro Ser Leu Leu Leu Leu Leu Glu Gly Thr Arg Trp Gln Ala Leu Val	

180	185	190	
cag gtg cag ccc agt gtg gac ccc acc aat gcc aca ggc ctc gat ggg Gln Val Gln Pro Ser Val Asp Pro Thr Asn Ala Thr Gly Leu Asp Gly 195 200 205			624
agg gag gca gct cct cac ttt ttg cag ggt ctg ttg ggt ttg ctt acc Arg Glu Ala Ala Pro His Phe Leu Gln Gly Leu Leu Gly Leu Leu Thr 210 215 220			672
cca aca ggg gag cta ggc tcc aag gag gct ctt tgg ggc ggt ctg cta Pro Thr Gly Glu Leu Gly Ser Lys Glu Ala Leu Trp Gly Gly Leu Leu 225 230 235 240			720
cgc aca gtg ggg gcc ccc ctc tat gct gcc ttt cag gag ggg ctg ctc Arg Thr Val Gly Ala Pro Leu Tyr Ala Ala Phe Gln Glu Gly Leu Leu 245 250 255			768
cgt gtc act cac tcc ctg cag gat gag gtc ttc tcc att ttg ggg cag Arg Val Thr His Ser Leu Gln Asp Glu Val Phe Ser Ile Leu Gly Gln 260 265 270			816
cca gag cct gat acc aat ggg cag tgc cag gga ggt aac ctt caa cag Pro Glu Pro Asp Thr Asn Gly Gln Cys Gln Gly Gly Asn Leu Gln Gln 275 280 285			864
ctg ctc tta tgg ggc gtc cgg cac aac ctt tcc tgg gat gtc cag gcg Leu Leu Leu Trp Gly Val Arg His Asn Leu Ser Trp Asp Val Gln Ala 290 295 300			912
ctg ggc ttt ctg tct gga tca cca ccc cca ccc cct gcc ctc ctt cac Leu Gly Phe Leu Ser Gly Ser Pro Pro Pro Pro Pro Ala Leu Leu His 305 310 315 320			960
tgc ctg agc acg ggc gtg cct ctg ccc aga gct tct cag ccg tca gcc Cys Leu Ser Thr Gly Val Pro Leu Pro Arg Ala Ser Gln Pro Ser Ala 325 330 335			1008
cac atc agc cca cgc caa cgg cga gcc atc act gtg gag gcc ctc tgt His Ile Ser Pro Arg Gln Arg Arg Ala Ile Thr Val Glu Ala Leu Cys 340 345 350			1056
gag aac cac tta ggc cca gca cca ccc tac agc att tcc aac ttc tcc			1104

Glu Asn His Leu Gly Pro Ala Pro Pro Tyr Ser Ile Ser Asn Phe Ser	
355 360 365	
atc cac ttg ctc tgc cag cac acc aag cct gcc act cca cag ccc cat	1152
Ile His Leu Leu Cys Gln His Thr Lys Pro Ala Thr Pro Gln Pro His	
370 375 380	
ccc agc acc act gcc atc tgc cag aca gct gtg tgg tat gca gtg tcc	1200
Pro Ser Thr Thr Ala Ile Cys Gln Thr Ala Val Trp Tyr Ala Val Ser	
385 390 395 400	
tgg gca cca ggt gcc caa ggc tgg cta cag gcc tgc cac gac cag ttt	1248
Trp Ala Pro Gly Ala Gln Gly Trp Leu Gln Ala Cys His Asp Gln Phe	
405 410 415	
cct gat gag ttt ttg gat gcg atc tgc agt aac ctc tcc ttt tca gcc	1296
Pro Asp Glu Phe Leu Asp Ala Ile Cys Ser Asn Leu Ser Phe Ser Ala	
420 425 430	
ctg tct ggc tcc aac cgc cgc ctg gtg aag cgg ctc tgt gct ggc ctg	1344
Leu Ser Gly Ser Asn Arg Arg Leu Val Lys Arg Leu Cys Ala Gly Leu	
435 440 445	
ctc cca ccc cct acc agc tgc cct gaa ggc ctg ccc cct gtt ccc ctc	1392
Leu Pro Pro Pro Thr Ser Cys Pro Glu Gly Leu Pro Pro Val Pro Leu	
450 455 460	
acc cca gac atc ttt tgg ggc tgc ttc ttg gag aat gag act ctg tgg	1440
Thr Pro Asp Ile Phe Trp Gly Cys Phe Leu Glu Asn Glu Thr Leu Trp	
465 470 475 480	
gct gag cga ctg tgt ggg gag gca agt cta cag gct gtg ccc ccc agc	1488
Ala Glu Arg Leu Cys Gly Glu Ala Ser Leu Gln Ala Val Pro Pro Ser	
485 490 495	
aac cag gct tgg gtc cag cat gtg tgc cag ggc ccc acc cca gat gtc	1536
Asn Gln Ala Trp Val Gln His Val Cys Gln Gly Pro Thr Pro Asp Val	
500 505 510	
act gcc tcc cca cca tgc cac att gga ccc tgt ggg gaa cgc tgc ccg	1584
Thr Ala Ser Pro Pro Cys His Ile Gly Pro Cys Gly Glu Arg Cys Pro	
515 520 525	

gat ggg ggc agc ttc ctg gtg atg gtc tgt gcc aat gac acc atg tat	1632
Asp Gly Gly Ser Phe Leu Val Met Val Cys Ala Asn Asp Thr Met Tyr	
530 535 540	
gag gtc ctg gtg ccc ttc tgg cct tgg cta gca ggc caa tgc agg ata	1680
Glu Val Leu Val Pro Phe Trp Pro Trp Leu Ala Gly Gln Cys Arg Ile	
545 550 555 560	
agt cgt ggg ggc aat gac act tgc ttc cta gaa ggg ctg ctg ggc ccc	1728
Ser Arg Gly Gly Asn Asp Thr Cys Phe Leu Glu Gly Leu Leu Gly Pro	
565 570 575	
ctt ctg ccc tct ctg cca cca ctg gga cca tcc cca ctc tgt ctg acc	1776
Leu Leu Pro Ser Leu Pro Pro Leu Gly Pro Ser Pro Leu Cys Leu Thr	
580 585 590	
cct ggc ccc ttc ctc ctt ggc atg cta tcc cag ttg cca cgc tgt cag	1824
Pro Gly Pro Phe Leu Leu Gly Met Leu Ser Gln Leu Pro Arg Cys Gln	
595 600 605	
tcc tct gtc cca gct ctt gct cac ccc aca cgc cta cac tat ctc ctc	1872
Ser Ser Val Pro Ala Leu Ala His Pro Thr Arg Leu His Tyr Leu Leu	
610 615 620	
cgc ctg ctg acc ttc ctc ttg ggt cca ggg gct ggg ggc gct gag gcc	1920
Arg Leu Leu Thr Phe Leu Leu Gly Pro Gly Ala Gly Gly Ala Glu Ala	
625 630 635 640	
cag ggg atg ctg ggt cgg gcc cta ctg ctc tcc agt ctc cca gac aac	1968
Gln Gly Met Leu Gly Arg Ala Leu Leu Leu Ser Ser Leu Pro Asp Asn	
645 650 655	
tgc tcc ttc tgg gat gcc ttt cgc cca gag ggc cgg cgc agt gtg cta	2016
Cys Ser Phe Trp Asp Ala Phe Arg Pro Glu Gly Arg Arg Ser Val Leu	
660 665 670	
cgg acg att ggg gaa tac ctg gaa caa gat gag gag cag cca acc cca	2064
Arg Thr Ile Gly Glu Tyr Leu Glu Gln Asp Glu Glu Gln Pro Thr Pro	
675 680 685	
tca ggc ttt gaa ccc act gtc aac ccc agc tct ggt ata agc aag atg	2112
Ser Gly Phe Glu Pro Thr Val Asn Pro Ser Ser Gly Ile Ser Lys Met	
690 695 700	

gag ctg ctg gcc tgc ttt agt gtg agt gct ctg cca gag gga aag ctc 2160
 Glu Leu Leu Ala Cys Phe Ser Val Ser Ala Leu Pro Glu Gly Lys Leu
 705 710 715 720

cta gaa cag tga 2172
 Leu Glu Gln *

<210> 100
 <211> 723
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Ser Phe Ala Val Thr Leu Ala Pro Thr Gly Pro His Ser Leu
 20 25 30
 Asp Pro Gly Leu Ser Phe Leu Lys Ser Leu Leu Ser Thr Leu Asp Gln
 35 40 45
 Ala Pro Gln Gly Ser Leu Ser Arg Ser Arg Phe Phe Thr Phe Leu Ala
 50 55 60
 Asn Ile Ser Ser Ser Phe Glu Pro Gly Arg Met Gly Glu Gly Pro Val
 65 70 75 80
 Gly Glu Pro Pro Pro Leu Gln Pro Pro Ala Leu Arg Leu His Asp Phe
 85 90 95
 Leu Val Thr Leu Arg Gly Ser Pro Asp Trp Glu Pro Met Leu Gly Leu
 100 105 110
 Leu Gly Asp Met Leu Ala Leu Leu Gly Gln Glu Gln Thr Pro Arg Asp
 115 120 125
 Phe Leu Val His Gln Ala Gly Val Leu Gly Gly Leu Val Glu Val Leu
 130 135 140
 Leu Gly Ala Leu Val Pro Gly Gly Pro Pro Thr Pro Thr Arg Pro Pro
 145 150 155 160
 Cys Thr Arg Asp Gly Pro Ser Asp Cys Val Leu Ala Ala Asp Trp Leu
 165 170 175
 Pro Ser Leu Leu Leu Leu Glu Gly Thr Arg Trp Gln Ala Leu Val
 180 185 190
 Gln Val Gln Pro Ser Val Asp Pro Thr Asn Ala Thr Gly Leu Asp Gly
 195 200 205
 Arg Glu Ala Ala Pro His Phe Leu Gln Gly Leu Leu Gly Leu Leu Thr

210 215 220
 Pro Thr Gly Glu Leu Gly Ser Lys Glu Ala Leu Trp Gly Gly Leu Leu
 225 230 235 240
 Arg Thr Val Gly Ala Pro Leu Tyr Ala Ala Phe Gln Glu Gly Leu Leu
 245 250 255
 Arg Val Thr His Ser Leu Gln Asp Glu Val Phe Ser Ile Leu Gly Gln
 260 265 270
 Pro Glu Pro Asp Thr Asn Gly Gln Cys Gln Gly Gly Asn Leu Gln Gln
 275 280 285
 Leu Leu Leu Trp Gly Val Arg His Asn Leu Ser Trp Asp Val Gln Ala
 290 295 300
 Leu Gly Phe Leu Ser Gly Ser Pro Pro Pro Pro Pro Ala Leu Leu His
 305 310 315 320
 Cys Leu Ser Thr Gly Val Pro Leu Pro Arg Ala Ser Gln Pro Ser Ala
 325 330 335
 His Ile Ser Pro Arg Gln Arg Arg Ala Ile Thr Val Glu Ala Leu Cys
 340 345 350
 Glu Asn His Leu Gly Pro Ala Pro Pro Tyr Ser Ile Ser Asn Phe Ser
 355 360 365
 Ile His Leu Leu Cys Gln His Thr Lys Pro Ala Thr Pro Gln Pro His
 370 375 380
 Pro Ser Thr Thr Ala Ile Cys Gln Thr Ala Val Trp Tyr Ala Val Ser
 385 390 395 400
 Trp Ala Pro Gly Ala Gln Gly Trp Leu Gln Ala Cys His Asp Gln Phe
 405 410 415
 Pro Asp Glu Phe Leu Asp Ala Ile Cys Ser Asn Leu Ser Phe Ser Ala
 420 425 430
 Leu Ser Gly Ser Asn Arg Arg Leu Val Lys Arg Leu Cys Ala Gly Leu
 435 440 445
 Leu Pro Pro Pro Thr Ser Cys Pro Glu Gly Leu Pro Pro Val Pro Leu
 450 455 460
 Thr Pro Asp Ile Phe Trp Gly Cys Phe Leu Glu Asn Glu Thr Leu Trp
 465 470 475 480
 Ala Glu Arg Leu Cys Gly Glu Ala Ser Leu Gln Ala Val Pro Pro Ser
 485 490 495
 Asn Gln Ala Trp Val Gln His Val Cys Gln Gly Pro Thr Pro Asp Val
 500 505 510
 Thr Ala Ser Pro Pro Cys His Ile Gly Pro Cys Gly Glu Arg Cys Pro
 515 520 525
 Asp Gly Gly Ser Phe Leu Val Met Val Cys Ala Asn Asp Thr Met Tyr
 530 535 540
 Glu Val Leu Val Pro Phe Trp Pro Trp Leu Ala Gly Gln Cys Arg Ile
 545 550 555 560

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<210> 101
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(456)

<400> 101
atg ctg agc agc cag tat ggg ctg atc gtg ttc gtg gcg ggg ctg ctg      48
Met Leu Ser Ser Gln Tyr Gly Leu Ile Val Phe Val Ala Gly Leu Leu
  1                5                10                15

ctg ctg ctg gcc tgg gcc gtt cga ccg cgg gca tgc tgt ggt acg tgg      96
Leu Leu Leu Ala Trp Ala Val Arg Pro Arg Ala Cys Cys Gly Thr Trp
      20                25                30

gcc gca ctc cgg aac cgc cgc ctc ttc cgc ctc aag gac acg cac gcc      144
Ala Ala Leu Arg Asn Arg Arg Leu Phe Arg Leu Lys Asp Thr His Ala

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<210> 102
<211> 151
<212> PRT
<213> Homo sapiens

<400> 102
Met Leu Ser Ser Gln Tyr Gly Leu Ile Val Phe Val Ala Gly Leu Leu
1 5 10 15
Leu Leu Leu Ala Trp Ala Val Arg Pro Arg Ala Cys Cys Gly Thr Trp
20 25 30
Ala Ala Leu Arg Asn Arg Arg Leu Phe Arg Leu Lys Asp Thr His Ala
35 40 45

Gly Ala Gly Trp Leu His Arg Leu Glu Pro Pro Leu Arg Leu Gln Thr
 50 55 60
 Leu Pro Ser Leu Gln Pro Gln Leu Gln Lys Pro Leu Leu Ser Phe Pro
 65 70 75 80
 Gly Leu Lys Pro Tyr Ser Gly Pro Thr Asp Pro Met Arg Glu Phe Ser
 85 90 95
 Ser Val Ala Asp Val Leu Trp Leu Gln Ala Ala Lys Cys Cys Phe Pro
 100 105 110
 Leu Leu Val Lys Glu Pro Ser Asn Pro Ser Asp Leu Pro Ser Arg Ala
 115 120 125
 Arg Ser Gly Pro Ser Ser Asn His Leu Gly Ala Ala Gly Arg Leu Leu
 130 135 140
 Tyr Ser Ala Arg Lys Glu Glu
 145 150

<210> 103
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(414)

<400> 103
 atg ggg cga gtc cgg acc ttg gcg ggc gag tgc tcg gcg cag gcg caa 48
 Met Gly Arg Val Arg Thr Leu Ala Gly Glu Cys Ser Ala Gln Ala Gln
 1 5 10 15
 gcg cag agt ctc ctc gcg gtc gtc ctt ttg gcc cct ccc ctc tgg ggg 96
 Ala Gln Ser Leu Leu Ala Val Val Leu Leu Ala Pro Pro Leu Trp Gly
 20 25 30
 acc ccc agt gcc agg ctg tca gtg cgc agc ccc cag cct gcg gga ccc 144
 Thr Pro Ser Ala Arg Leu Ser Val Arg Ser Pro Gln Pro Ala Gly Pro
 35 40 45
 ctg ggg act ctg ggc gcc tgt tct gca aat gac cgg ttc tta cga gtt 192
 Leu Gly Thr Leu Gly Ala Cys Ser Ala Asn Asp Arg Phe Leu Arg Val
 50 55 60
 caa gct gaa cca gcc acc cga gga tgg cat ctc ctc cgt gaa gtt aag 240
 Gln Ala Glu Pro Ala Thr Arg Gly Trp His Leu Leu Arg Glu Val Lys

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<210> 104
<211> 137
<212> PRT
<213> Homo sapiens

<400> 104
Met Gly Arg Val Arg Thr Leu Ala Gly Glu Cys Ser Ala Gln Ala Gln
 1          5          10          15
Ala Gln Ser Leu Leu Ala Val Val Leu Leu Ala Pro Pro Leu Trp Gly
          20          25          30
Thr Pro Ser Ala Arg Leu Ser Val Arg Ser Pro Gln Pro Ala Gly Pro
          35          40          45
Leu Gly Thr Leu Gly Ala Cys Ser Ala Asn Asp Arg Phe Leu Arg Val
 50          55          60
Gln Ala Glu Pro Ala Thr Arg Gly Trp His Leu Leu Arg Glu Val Lys
65          70          75          80
Pro Pro His Pro Ser Gln Ser Trp Val Val Ser Phe Leu Gly Asp Val
          85          90          95
Pro Cys Val Phe Thr Met Trp Pro Gly Asn Phe Met Ala Val Lys Tyr
          100          105          110
Gln Ala His Arg Gly Pro Ser Trp Glu Trp Ala Phe Leu Ile Ser Ile
          115          120          125
Tyr Pro Leu Gly Arg Arg Val Lys Cys
          130          135

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<210> 105
 <211> 1260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1260)

<400> 105

atg ggg ccc atg ctg ctg cct ctg gct ctg ctg gcc ctg ctg ctg ggg	48
Met Gly Pro Met Leu Leu Pro Leu Ala Leu Leu Ala Leu Leu Leu Gly	
1 5 10 15	
cct gcg ctg gcc cgg agt gcc cgg gac ccg gag gtg ttc tgt gga ggc	96
Pro Ala Leu Ala Arg Ser Ala Arg Asp Pro Glu Val Phe Cys Gly Gly	
20 25 30	
gtc ata tta gca ata aaa tgc atg aaa cca gca ttc ttt gcc acc ttc	144
Val Ile Leu Ala Ile Lys Cys Met Lys Pro Ala Phe Phe Ala Thr Phe	
35 40 45	
tcg cta atc att gct att ttc tcg gag aga gag gct ctt ggc aaa ggt	192
Ser Leu Ile Ile Ala Ile Phe Ser Glu Arg Glu Ala Leu Gly Lys Gly	
50 55 60	
cac agc cct gga ccc ggt ttt cct tcc tgg aat att tgg gtg gtg aca	240
His Ser Pro Gly Pro Gly Phe Pro Ser Trp Asn Ile Trp Val Val Thr	
65 70 75 80	
tcg cag ctg agc ccc ttc cat gga att ctg tgg tgt tgg gct gtt ctt	288
Ser Gln Leu Ser Pro Phe His Gly Ile Leu Trp Cys Trp Ala Val Leu	
85 90 95	
caa gag aag att agg aca cag aca cac aca gag gga cgg cca cgt gag	336
Gln Glu Lys Ile Arg Thr Gln Thr His Thr Glu Gly Arg Pro Arg Glu	
100 105 110	
gac ata ggg aga aga cag ctg tct gca agt caa gga ggg gcc tca gaa	384
Asp Ile Gly Arg Arg Gln Leu Ser Ala Ser Gln Gly Gly Ala Ser Glu	
115 120 125	

gga acc aac cct cct gac acc ttg atc ttg gac ttc cag ctg cag aac	432
Gly Thr Asn Pro Pro Asp Thr Leu Ile Leu Asp Phe Gln Leu Gln Asn	
130 135 140	
ggg tgt ttt ggc aaa tac acc ttc atc tgc tct tca cct ggt aaa tgc	480
Gly Cys Phe Gly Lys Tyr Thr Phe Ile Cys Ser Ser Pro Gly Lys Cys	
145 150 155 160	
ctg atc atc ttt cag gtc cta ctt gtc atg ctc tta ggg aag cct ccc	528
Leu Ile Ile Phe Gln Val Leu Leu Val Met Leu Leu Gly Lys Pro Pro	
165 170 175	
gtg ttc ttt gac aag aag gtc ccg tcg gtg gat caa ggc cct ccc tac	576
Val Phe Phe Asp Lys Lys Val Pro Ser Val Asp Gln Gly Pro Pro Tyr	
180 185 190	
tcc agt atg act tgg tct gaa tca atc cca tct gca aag acc cta ttc	624
Ser Ser Met Thr Trp Ser Glu Ser Ile Pro Ser Ala Lys Thr Leu Phe	
195 200 205	
cca aat aag gcc aca ttc aca gcg tgc agg gcg ctg atg gac gag ata	672
Pro Asn Lys Ala Thr Phe Thr Ala Cys Arg Ala Leu Met Asp Glu Ile	
210 215 220	
gag cac gac atc acc aag gct cgg cag aag aag acc aag gtg gga tcc	720
Glu His Asp Ile Thr Lys Ala Arg Gln Lys Lys Thr Lys Val Gly Ser	
225 230 235 240	
ttc cga atc aat ccc gat ggg act cag gag agg aga aag cac cta aat	768
Phe Arg Ile Asn Pro Asp Gly Thr Gln Glu Arg Arg Lys His Leu Asn	
245 250 255	
ttt gtg tct cgt caa gtc gaa aga cat ttc ggc act gtt ctt cat cag	816
Phe Val Ser Arg Gln Val Glu Arg His Phe Gly Thr Val Leu His Gln	
260 265 270	
aat aaa aat agc gcg tct gtg gtt ctt ggc aca ctc aag gat gga tcc	864
Asn Lys Asn Ser Ala Ser Val Val Leu Gly Thr Leu Lys Asp Gly Ser	
275 280 285	
ttc aag agc cgt gtc tgg caa gtc cac cgg agg gac ccc gtg cag gcc	912
Phe Lys Ser Arg Val Trp Gln Val His Arg Arg Asp Pro Val Gln Ala	
290 295 300	

cac tgg ctg ctc tgc tgc agg tct gac gcc tgc acc ccg gaa tct caa 960
 His Trp Leu Leu Cys Cys Arg Ser Asp Ala Cys Thr Pro Glu Ser Gln
 305 310 315 320

ggt cct ttg tgg tca cct gaa tgc agg aca tgt gcc tcc ata aaa tcc 1008
 Gly Pro Leu Trp Ser Pro Glu Cys Arg Thr Cys Ala Ser Ile Lys Ser
 325 330 335

agt aca gtc ctg gtc cct gac acc agc cgg gag ctg att ccc act gtc 1056
 Ser Thr Val Leu Val Pro Asp Thr Ser Arg Glu Leu Ile Pro Thr Val
 340 345 350

aag cag ggc cag gga aga tca ttc cgg gtc tac atg tgg tgt gga cta 1104
 Lys Gln Gly Gln Gly Arg Ser Phe Arg Val Tyr Met Trp Cys Gly Leu
 355 360 365

ggg gag gaa ttc ttc ccc cat agg agc tca cac tct gac cca gag acc 1152
 Gly Glu Glu Phe Phe Pro His Arg Ser Ser His Ser Asp Pro Glu Thr
 370 375 380

tca gca gcc gcc agt gtg aac gcc acg tct cag aga gtg aag gga ggg 1200
 Ser Ala Ala Ala Ser Val Asn Ala Thr Ser Gln Arg Val Lys Gly Gly
 385 390 395 400

agc ctc agg aaa tac act gag aca ata gtc aca gtt ctt gta tct gcg 1248
 Ser Leu Arg Lys Tyr Thr Glu Thr Ile Val Thr Val Leu Val Ser Ala
 405 410 415

tat tac tgc tga 1260
 Tyr Tyr Cys *

<210> 106

<211> 419

<212> PRT

<213> Homo sapiens

<400> 106

Met Gly Pro Met Leu Leu Pro Leu Ala Leu Leu Ala Leu Leu Leu Gly
 1 5 10 15
 Pro Ala Leu Ala Arg Ser Ala Arg Asp Pro Glu Val Phe Cys Gly Gly

20 25 30
 Val Ile Leu Ala Ile Lys Cys Met Lys Pro Ala Phe Phe Ala Thr Phe
 35 40 45
 Ser Leu Ile Ile Ala Ile Phe Ser Glu Arg Glu Ala Leu Gly Lys Gly
 50 55 60
 His Ser Pro Gly Pro Gly Phe Pro Ser Trp Asn Ile Trp Val Val Thr
 65 70 75 80
 Ser Gln Leu Ser Pro Phe His Gly Ile Leu Trp Cys Trp Ala Val Leu
 85 90 95
 Gln Glu Lys Ile Arg Thr Gln Thr His Thr Glu Gly Arg Pro Arg Glu
 100 105 110
 Asp Ile Gly Arg Arg Gln Leu Ser Ala Ser Gln Gly Gly Ala Ser Glu
 115 120 125
 Gly Thr Asn Pro Pro Asp Thr Leu Ile Leu Asp Phe Gln Leu Gln Asn
 130 135 140
 Gly Cys Phe Gly Lys Tyr Thr Phe Ile Cys Ser Ser Pro Gly Lys Cys
 145 150 155 160
 Leu Ile Ile Phe Gln Val Leu Leu Val Met Leu Leu Gly Lys Pro Pro
 165 170 175
 Val Phe Phe Asp Lys Lys Val Pro Ser Val Asp Gln Gly Pro Pro Tyr
 180 185 190
 Ser Ser Met Thr Trp Ser Glu Ser Ile Pro Ser Ala Lys Thr Leu Phe
 195 200 205
 Pro Asn Lys Ala Thr Phe Thr Ala Cys Arg Ala Leu Met Asp Glu Ile
 210 215 220
 Glu His Asp Ile Thr Lys Ala Arg Gln Lys Lys Thr Lys Val Gly Ser
 225 230 235 240
 Phe Arg Ile Asn Pro Asp Gly Thr Gln Glu Arg Arg Lys His Leu Asn
 245 250 255
 Phe Val Ser Arg Gln Val Glu Arg His Phe Gly Thr Val Leu His Gln
 260 265 270
 Asn Lys Asn Ser Ala Ser Val Val Leu Gly Thr Leu Lys Asp Gly Ser
 275 280 285
 Phe Lys Ser Arg Val Trp Gln Val His Arg Arg Asp Pro Val Gln Ala
 290 295 300
 His Trp Leu Leu Cys Cys Arg Ser Asp Ala Cys Thr Pro Glu Ser Gln
 305 310 315 320
 Gly Pro Leu Trp Ser Pro Glu Cys Arg Thr Cys Ala Ser Ile Lys Ser
 325 330 335
 Ser Thr Val Leu Val Pro Asp Thr Ser Arg Glu Leu Ile Pro Thr Val
 340 345 350
 Lys Gln Gly Gln Gly Arg Ser Phe Arg Val Tyr Met Trp Cys Gly Leu
 355 360 365

Gly Glu Glu Phe Phe Pro His Arg Ser Ser His Ser Asp Pro Glu Thr
 370 375 380
 Ser Ala Ala Ala Ser Val Asn Ala Thr Ser Gln Arg Val Lys Gly Gly
 385 390 395 400
 Ser Leu Arg Lys Tyr Thr Glu Thr Ile Val Thr Val Leu Val Ser Ala
 405 410 415
 Tyr Tyr Cys

<210> 107
 <211> 669
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(669)

<400> 107
 atg gcg cct cct ctg cga ccc ctc gcc cgg ctg cga ccg ccg ggg atg 48
 Met Ala Pro Pro Leu Arg Pro Leu Ala Arg Leu Arg Pro Pro Gly Met
 1 5 10 15
 ctg ctc cgc gcg ctc ctg ctc ctg ctg ctg ctc agt cct ttg cca ggg 96
 Leu Leu Arg Ala Leu Leu Leu Leu Leu Leu Ser Pro Leu Pro Gly
 20 25 30
 ctg cga gag gga ata ggt gaa ctc ata acc cca atc ggc acc agc ttg 144
 Leu Arg Glu Gly Ile Gly Glu Leu Ile Thr Pro Ile Gly Thr Ser Leu
 35 40 45
 ccg gat ctg gat cca gcc agg agg aga tgg gag ggt gga att ggc agg 192
 Pro Asp Leu Asp Pro Ala Arg Arg Arg Trp Glu Gly Gly Ile Gly Arg
 50 55 60
 gtt gga agt gaa gtg gcc gat ttg tgc ccc gga aag gag ggg gga aaa 240
 Val Gly Ser Glu Val Ala Asp Leu Cys Pro Gly Lys Glu Gly Gly Lys
 65 70 75 80
 gtc ccc gaa gct gaa aag gaa gga gtg tgg tgc ttt agc gaa ctg tct 288
 Val Pro Glu Ala Glu Lys Glu Gly Val Trp Cys Phe Ser Glu Leu Ser
 85 90 95

ttt gta aaa gaa cca cag gat gta act gtc aca aga aag gac cca gtc 336
 Phe Val Lys Glu Pro Gln Asp Val Thr Val Thr Arg Lys Asp Pro Val
 100 105 110

gtt tta gat tgc cag gct cac gga gaa gtt cct att aag gtc aca tgg 384
 Val Leu Asp Cys Gln Ala His Gly Glu Val Pro Ile Lys Val Thr Trp
 115 120 125

ttg aaa aat gga gca aaa atg tct gaa aat aaa cgg atc gag gtt ctt 432
 Leu Lys Asn Gly Ala Lys Met Ser Glu Asn Lys Arg Ile Glu Val Leu
 130 135 140

tct aac ggc tct tta tac atc agt gag gtg gaa ggc agg cga gga gag 480
 Ser Asn Gly Ser Leu Tyr Ile Ser Glu Val Glu Gly Arg Arg Gly Glu
 145 150 155 160

cag tcc gat gaa gga ttt tat cag tgc ttg gca atg aac aaa tat gga 528
 Gln Ser Asp Glu Gly Phe Tyr Gln Cys Leu Ala Met Asn Lys Tyr Gly
 165 170 175

gcc att ctt agt caa aaa gct cat ctt gcc tta tca atg tta gcg gca 576
 Ala Ile Leu Ser Gln Lys Ala His Leu Ala Leu Ser Met Leu Ala Ala
 180 185 190

tcc ctg gcc tct acc ctc cca ata ccg ata gac tct ctt cca gtt gtg 624
 Ser Leu Ala Ser Thr Leu Pro Ile Pro Ile Asp Ser Leu Pro Val Val
 195 200 205

aca acc aag aaa gtt cta ctg tgg ggc aaa ata act cct gat tga 669
 Thr Thr Lys Lys Val Leu Leu Trp Gly Lys Ile Thr Pro Asp *
 210 215 220

<210> 108

<211> 222

<212> PRT

<213> Homo sapiens

<400> 108

Met Ala Pro Pro Leu Arg Pro Leu Ala Arg Leu Arg Pro Pro Gly Met
 1 5 10 15
 Leu Leu Arg Ala Leu Leu Leu Leu Leu Leu Ser Pro Leu Pro Gly
 20 25 30

Leu Arg Glu Gly Ile Gly Glu Leu Ile Thr Pro Ile Gly Thr Ser Leu
 35 40 45
 Pro Asp Leu Asp Pro Ala Arg Arg Arg Trp Glu Gly Gly Ile Gly Arg
 50 55 60
 Val Gly Ser Glu Val Ala Asp Leu Cys Pro Gly Lys Glu Gly Gly Lys
 65 70 75 80
 Val Pro Glu Ala Glu Lys Glu Gly Val Trp Cys Phe Ser Glu Leu Ser
 85 90 95
 Phe Val Lys Glu Pro Gln Asp Val Thr Val Thr Arg Lys Asp Pro Val
 100 105 110
 Val Leu Asp Cys Gln Ala His Gly Glu Val Pro Ile Lys Val Thr Trp
 115 120 125
 Leu Lys Asn Gly Ala Lys Met Ser Glu Asn Lys Arg Ile Glu Val Leu
 130 135 140
 Ser Asn Gly Ser Leu Tyr Ile Ser Glu Val Glu Gly Arg Arg Gly Glu
 145 150 155 160
 Gln Ser Asp Glu Gly Phe Tyr Gln Cys Leu Ala Met Asn Lys Tyr Gly
 165 170 175
 Ala Ile Leu Ser Gln Lys Ala His Leu Ala Leu Ser Met Leu Ala Ala
 180 185 190
 Ser Leu Ala Ser Thr Leu Pro Ile Pro Ile Asp Ser Leu Pro Val Val
 195 200 205
 Thr Thr Lys Lys Val Leu Leu Trp Gly Lys Ile Thr Pro Asp
 210 215 220

<210> 109

<211> 864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(864)

<400> 109

atg cgg caa acc cta ccg ctg ctg ctg ctg acg gtg ctg cgc ccc agc
 Met Arg Gln Thr Leu Pro Leu Leu Leu Leu Thr Val Leu Arg Pro Ser
 1 5 10 15

48

tgg gca gac cct ccc cag gag aag gtc ccg ctc ttc cgg gtc act cag
 Trp Ala Asp Pro Pro Gln Glu Lys Val Pro Leu Phe Arg Val Thr Gln
 20 25 30

96

cag ggc ccc tgg ggg agc agt ggc agc aac gcc acc gac tcg ccc tgc	144
Gln Gly Pro Trp Gly Ser Ser Gly Ser Asn Ala Thr Asp Ser Pro Cys	
35 40 45	
gag ggg ctg ccc gcc gcg gat gcg acg gcc ttg acc ctg gcg aac cgc	192
Glu Gly Leu Pro Ala Ala Asp Ala Thr Ala Leu Thr Leu Ala Asn Arg	
50 55 60	
aac ctg gag cgc ctg ccc ggc tgc cta ccg cgc aca ctg cgc agc ctc	240
Asn Leu Glu Arg Leu Pro Gly Cys Leu Pro Arg Thr Leu Arg Ser Leu	
65 70 75 80	
gac gcc agc cac aac ctg ctg cgc gcc ctg agc act tcc gag ctc ggc	288
Asp Ala Ser His Asn Leu Leu Arg Ala Leu Ser Thr Ser Glu Leu Gly	
85 90 95	
cac ctg gag cag ctg cag gtg ctg acc ctg cgc cac aac cgc atc gcc	336
His Leu Glu Gln Leu Gln Val Leu Thr Leu Arg His Asn Arg Ile Ala	
100 105 110	
gcg ctg cgc tgg ggc ccg ggt ggg ccg gcg ggg ctg cac acc ctg gac	384
Ala Leu Arg Trp Gly Pro Gly Gly Pro Ala Gly Leu His Thr Leu Asp	
115 120 125	
ctc agc tac aac cag ctg gcc gct ctg ccg ccg tgc acc ggg ccc gcg	432
Leu Ser Tyr Asn Gln Leu Ala Ala Leu Pro Pro Cys Thr Gly Pro Ala	
130 135 140	
ctg agc agc ctc cgc gcc ctg gcg ctc gcc ggg aat ccg ctg cgg gcg	480
Leu Ser Ser Leu Arg Ala Leu Ala Leu Ala Gly Asn Pro Leu Arg Ala	
145 150 155 160	
ctg cag ccc cgg gcc ttc gcc tgc ttc ccc gcg ctg cag ctc ctc aac	528
Leu Gln Pro Arg Ala Phe Ala Cys Phe Pro Ala Leu Gln Leu Leu Asn	
165 170 175	
ctc tcc tgc acc gcg ctg ggt cgc gga gcc cag ggg ggc atc gcc gag	576
Leu Ser Cys Thr Ala Leu Gly Arg Gly Ala Gln Gly Gly Ile Ala Glu	
180 185 190	
gcg gcg ttc gct gga gag gat ggc gcg ccc ctg gtc acg ctc gaa gtc	624
Ala Ala Phe Ala Gly Glu Asp Gly Ala Pro Leu Val Thr Leu Glu Val	
195 200 205	

ctg gat ctc agc ggc acg ttc ctt gaa cgg gtt gag tca ggg tgg atc 672
 Leu Asp Leu Ser Gly Thr Phe Leu Glu Arg Val Glu Ser Gly Trp Ile
 210 215 220

aga gac ctg ccg aag ctc aca tcc ctc tac ctg agg aag atg cct cgg 720
 Arg Asp Leu Pro Lys Leu Thr Ser Leu Tyr Leu Arg Lys Met Pro Arg
 225 230 235 240

ctg acg acc ctg gag ggg gac att ttc aag atg acc ccc aac ctg cag 768
 Leu Thr Thr Leu Glu Gly Asp Ile Phe Lys Met Thr Pro Asn Leu Gln
 245 250 255

cag ctg gac tgt cag gac tcc cca gca ctt gct tct gtc gcc aca cac 816
 Gln Leu Asp Cys Gln Asp Ser Pro Ala Leu Ala Ser Val Ala Thr His
 260 265 270

atc ttt caa gat act cca cat cta cag gtc ctt ctg ttc cag aag taa 864
 Ile Phe Gln Asp Thr Pro His Leu Gln Val Leu Leu Phe Gln Lys *
 275 280 285

<210> 110

<211> 287

<212> PRT

<213> Homo sapiens

<400> 110

Met Arg Gln Thr Leu Pro Leu Leu Leu Leu Thr Val Leu Arg Pro Ser
 1 5 10 15
 Trp Ala Asp Pro Pro Gln Glu Lys Val Pro Leu Phe Arg Val Thr Gln
 20 25 30
 Gln Gly Pro Trp Gly Ser Ser Gly Ser Asn Ala Thr Asp Ser Pro Cys
 35 40 45
 Glu Gly Leu Pro Ala Ala Asp Ala Thr Ala Leu Thr Leu Ala Asn Arg
 50 55 60
 Asn Leu Glu Arg Leu Pro Gly Cys Leu Pro Arg Thr Leu Arg Ser Leu
 65 70 75 80
 Asp Ala Ser His Asn Leu Leu Arg Ala Leu Ser Thr Ser Glu Leu Gly
 85 90 95
 His Leu Glu Gln Leu Gln Val Leu Thr Leu Arg His Asn Arg Ile Ala
 100 105 110
 Ala Leu Arg Trp Gly Pro Gly Gly Pro Ala Gly Leu His Thr Leu Asp

115 120 125
 Leu Ser Tyr Asn Gln Leu Ala Ala Leu Pro Pro Cys Thr Gly Pro Ala
 130 135 140
 Leu Ser Ser Leu Arg Ala Leu Ala Leu Ala Gly Asn Pro Leu Arg Ala
 145 150 155 160
 Leu Gln Pro Arg Ala Phe Ala Cys Phe Pro Ala Leu Gln Leu Leu Asn
 165 170 175
 Leu Ser Cys Thr Ala Leu Gly Arg Gly Ala Gln Gly Gly Ile Ala Glu
 180 185 190
 Ala Ala Phe Ala Gly Glu Asp Gly Ala Pro Leu Val Thr Leu Glu Val
 195 200 205
 Leu Asp Leu Ser Gly Thr Phe Leu Glu Arg Val Glu Ser Gly Trp Ile
 210 215 220
 Arg Asp Leu Pro Lys Leu Thr Ser Leu Tyr Leu Arg Lys Met Pro Arg
 225 230 235 240
 Leu Thr Thr Leu Glu Gly Asp Ile Phe Lys Met Thr Pro Asn Leu Gln
 245 250 255
 Gln Leu Asp Cys Gln Asp Ser Pro Ala Leu Ala Ser Val Ala Thr His
 260 265 270
 Ile Phe Gln Asp Thr Pro His Leu Gln Val Leu Leu Phe Gln Lys
 275 280 285

<210> 111
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(603)

<400> 111
 atg gaa aag gaa tta atc ttc tca ccc tgg cga gtt ttc ctg aaa cta 48
 Met Glu Lys Glu Leu Ile Phe Ser Pro Trp Arg Val Phe Leu Lys Leu
 1 5 10 15
 ctt atc ctt agc gtc agc gct gta aga ggt gga gcc gct cag tcc cgc 96
 Leu Ile Leu Ser Val Ser Ala Val Arg Gly Gly Ala Ala Gln Ser Arg
 20 25 30
 ggg tgg ctg cag aca gaa ggg gta gtg gac agt gtt gac ttg aat tgc 144
 Gly Trp Leu Gln Thr Glu Gly Val Val Asp Ser Val Asp Leu Asn Cys
 35 40 45

tgt ccc tcg ttc caa gcc ttt cct gtg aat gaa ccc gaa aac act cga	192
Cys Pro Ser Phe Gln Ala Phe Pro Val Asn Glu Pro Glu Asn Thr Arg	
50 55 60	
cag gtc gtg aat aat cgt ttt aat gag tgt gca aag cgt gcg acg gga	240
Gln Val Val Asn Asn Arg Phe Asn Glu Cys Ala Lys Arg Ala Thr Gly	
65 70 75 80	
cac act ttc ggt ccc ccg cca gag ctc cgg tgc ccc cga gtg acc gct	288
His Thr Phe Gly Pro Pro Glu Leu Arg Cys Pro Arg Val Thr Ala	
85 90 95	
ttc tgc gat cgc gtc cgc cgg gac ccc gtc cct ctt tcc cct tca gtc	336
Phe Cys Asp Arg Val Arg Arg Asp Pro Val Pro Leu Ser Pro Ser Val	
100 105 110	
ttc agg gag ggg gag gcg ctc cgc att agc ggg gca gtt cag caa ccc	384
Phe Arg Glu Gly Glu Ala Leu Arg Ile Ser Gly Ala Val Gln Gln Pro	
115 120 125	
cga ccc cac ccg cgt ggc tcc agg ccc agg ggt ccg ttc act tcc ccg	432
Arg Pro His Pro Arg Gly Ser Arg Pro Arg Gly Pro Phe Thr Ser Pro	
130 135 140	
tcc ggt ttg ggg gac gcc aat tcg cct aag aaa acc ctg gca gaa gag	480
Ser Gly Leu Gly Asp Ala Asn Ser Pro Lys Lys Thr Leu Ala Glu Glu	
145 150 155 160	
cgc gga ccc ttc act aca aac ctc acg tca ggg tta cag cca cat tta	528
Arg Gly Pro Phe Thr Thr Asn Leu Thr Ser Gly Leu Gln Pro His Leu	
165 170 175	
gga acc tct tcg gaa aag ctg aga aat cac tgt ttt gca aaa agc ctt	576
Gly Thr Ser Ser Glu Lys Leu Arg Asn His Cys Phe Ala Lys Ser Leu	
180 185 190	
ctg tac tgt gat ggg gct ttg tgg tga	603
Leu Tyr Cys Asp Gly Ala Leu Trp *	
195 200	

<211> 200
 <212> PRT
 <213> Homo sapiens

<400> 112

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Met Glu Lys Glu Leu Ile Phe Ser Pro Trp Arg Val Phe Leu Lys Leu
 1           5           10           15
Leu Ile Leu Ser Val Ser Ala Val Arg Gly Gly Ala Ala Gln Ser Arg
 20           25           30
Gly Trp Leu Gln Thr Glu Gly Val Val Asp Ser Val Asp Leu Asn Cys
 35           40           45
Cys Pro Ser Phe Gln Ala Phe Pro Val Asn Glu Pro Glu Asn Thr Arg
 50           55           60
Gln Val Val Asn Asn Arg Phe Asn Glu Cys Ala Lys Arg Ala Thr Gly
 65           70           75           80
His Thr Phe Gly Pro Pro Glu Leu Arg Cys Pro Arg Val Thr Ala
 85           90           95
Phe Cys Asp Arg Val Arg Arg Asp Pro Val Pro Leu Ser Pro Ser Val
 100          105          110
Phe Arg Glu Gly Glu Ala Leu Arg Ile Ser Gly Ala Val Gln Gln Pro
 115          120          125
Arg Pro His Pro Arg Gly Ser Arg Pro Arg Gly Pro Phe Thr Ser Pro
 130          135          140
Ser Gly Leu Gly Asp Ala Asn Ser Pro Lys Lys Thr Leu Ala Glu Glu
 145          150          155          160
Arg Gly Pro Phe Thr Thr Asn Leu Thr Ser Gly Leu Gln Pro His Leu
 165          170          175
Gly Thr Ser Ser Glu Lys Leu Arg Asn His Cys Phe Ala Lys Ser Leu
 180          185          190
Leu Tyr Cys Asp Gly Ala Leu Trp
 195          200

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<210> 113
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(285)

<400> 113

atg gct tca gtg gcc tgg gcc gtc ctc aag gtg ctg ctg ctt ctc ccc

act cag act tgg agc ccc gta gga gca gga aat cca ctt agc tat tcg 96
Thr Gln Thr Trp Ser Pro Val Gly Ala Gly Asn Pro Leu Ser Tyr Ser
20 25 30

tct aat cct ttt tca agg ttt tta gct tct ttg cga cgg gtt cga aca 144
Ser Asn Pro Phe Ser Arg Phe Leu Ala Ser Leu Arg Arg Val Arg Thr
35 40 45

tcc tcc ttt agc tcg gag aag ttt gtt att acc gat cat ctg aaa cct 192
Ser Ser Phe Ser Ser Glu Lys Phe Val Ile Thr Asp His Leu Lys Pro
50 55 60

tct tct ctc aac tcg tca aag tca ttc tcc atc cag ctt tgt tcc gtt 240
Ser Ser Leu Asn Ser Ser Lys Ser Phe Ser Ile Gln Leu Cys Ser Val
65 70 75 80

gct ggc gag gcg ttg tgt tcc ttt gga gga gaa gag gcg ctc tga 285
Ala Gly Glu Ala Leu Cys Ser Phe Gly Gly Glu Glu Ala Leu *
85 90

<210> 114

<211> 94

<212> PRT

<213> Homo sapiens

<400> 114

Met	Ala	Ser	Val	Ala	Trp	Ala	Val	Leu	Lys	Val	Leu	Leu	Leu	Leu	Pro
1				5				10						15	
Thr	Gln	Thr	Trp	Ser	Pro	Val	Gly	Ala	Gly	Asn	Pro	Leu	Ser	Tyr	Ser
			20				25						30		
Ser	Asn	Pro	Phe	Ser	Arg	Phe	Leu	Ala	Ser	Leu	Arg	Arg	Val	Arg	Thr
		35					40					45			
Ser	Ser	Phe	Ser	Ser	Glu	Lys	Phe	Val	Ile	Thr	Asp	His	Leu	Lys	Pro
	50					55					60				
Ser	Ser	Leu	Asn	Ser	Ser	Lys	Ser	Phe	Ser	Ile	Gln	Leu	Cys	Ser	Val
65					70					75					80
Ala	Gly	Glu	Ala	Leu	Cys	Ser	Phe	Gly	Gly	Glu	Glu	Ala	Leu		
				85					90						

<400> 115

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<210> 116
<211> 103
<212> PRT
<213> Homo sapiens
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tcc ctc tct tca att cca tgg tat att ttg tcc ttc agt tct gca gag 240
 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80

 cct gca atc aaa cat gct aaa gca gag aaa tac aat aag aga cct ata 288
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95

 ctt gac att agc aga gga agt cca gct gtg tac act aat tat gat aaa 336
 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
 100 105 110

 cat cca ttc aca atg tct ggg agg aga cta gcc aca gac ctg gaa aga 384
 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
 115 120 125

 ggt gaa gaa aaa cga cac cat gaa aaa gga gca aag tga 423
 Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys *
 130 135 140

<210> 118
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 118
 Met Pro Pro Leu Leu Val Leu Leu Leu Leu Leu Pro Pro Pro Leu Ala
 1 5 10 15
 Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
 20 25 30
 Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
 35 40 45
 Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
 50 55 60
 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95
 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
 100 105 110
 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
 115 120 125

Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys
 130 135 140

<210> 119
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(336)

<400> 119

atg gga tgc aga ctg ctg acc ctg ctg tgt ttc cta caa cct gct tcc	48
Met Gly Cys Arg Leu Leu Thr Leu Leu Cys Phe Leu Gln Pro Ala Ser	
1 5 10 15	
agc tcc tcg tgg ctc ttt ggc tcc caa tcc aga gct ttc gcg aac acc	96
Ser Ser Ser Trp Leu Phe Gly Ser Gln Ser Arg Ala Phe Ala Asn Thr	
20 25 30	
aga gcc cct gtg cct ctc cct gca gct ggc tgg gag ttc cag ggc att	144
Arg Ala Val Pro Leu Pro Ala Ala Gly Trp Glu Phe Gln Gly Ile	
35 40 45	
aac aca gac agt ctt tgc cca tca gcc agt gac tgt atg gag ctt gga	192
Asn Thr Asp Ser Leu Cys Pro Ser Ala Ser Asp Cys Met Glu Leu Gly	
50 55 60	
tgt gaa tac aca gct cct gca tcc ctc cga ggc atc tcc aca ccg tct	240
Cys Glu Tyr Thr Ala Pro Ala Ser Leu Arg Gly Ile Ser Thr Pro Ser	
65 70 75 80	
ccc aga gaa tgt ctc gta aaa gct gct cct ctt ggg gag gct ctg ggc	288
Pro Arg Glu Cys Leu Val Lys Ala Ala Pro Leu Gly Glu Ala Leu Gly	
85 90 95	
ttt gga gag agc acc tgg aat tcc cca cta gaa aag ccc aaa aac tga	336
Phe Gly Glu Ser Thr Trp Asn Ser Pro Leu Glu Lys Pro Lys Asn *	
100 105 110	

<210> 120

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 120

Met Gly Cys Arg Leu Leu Thr Leu Leu Cys Phe Leu Gln Pro Ala Ser
 1 5 10 15
 Ser Ser Ser Trp Leu Phe Gly Ser Gln Ser Arg Ala Phe Ala Asn Thr
 20 25 30
 Arg Ala Pro Val Pro Leu Pro Ala Ala Gly Trp Glu Phe Gln Gly Ile
 35 40 45
 Asn Thr Asp Ser Leu Cys Pro Ser Ala Ser Asp Cys Met Glu Leu Gly
 50 55 60
 Cys Glu Tyr Thr Ala Pro Ala Ser Leu Arg Gly Ile Ser Thr Pro Ser
 65 70 75 80
 Pro Arg Glu Cys Leu Val Lys Ala Ala Pro Leu Gly Glu Ala Leu Gly
 85 90 95
 Phe Gly Glu Ser Thr Trp Asn Ser Pro Leu Glu Lys Pro Lys Asn
 100 105 110

<210> 121
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(336)

<400> 121

atg aag ctc ctt ctt ctg ctt ttg act gtt act ctg ctc ctg gcc cag 48
 Met Lys Leu Leu Leu Leu Leu Leu Thr Val Thr Leu Leu Leu Ala Gln
 1 5 10 15
 gtc acc cca ggt ctg cca gcc atg aaa ctt ctt tac ctg ttt ctt gcc 96
 Val Thr Pro Gly Leu Pro Ala Met Lys Leu Leu Tyr Leu Phe Leu Ala
 20 25 30
 atc ctt ctg gcc ata gaa gaa cca gtg ata tca gta gag tgt tgg atg 144
 Ile Leu Leu Ala Ile Glu Glu Pro Val Ile Ser Val Glu Cys Trp Met
 35 40 45
 gat gga cac tgc cgg ttg ttg tgc aaa gat ggt gaa gac agc atc ata 192

Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
 50 55 60

cgc tgc cga aat cgt aaa cgg tgc tgt gtt cct agt cgt tat tta aca 240
 Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
 65 70 75 80

atc caa cca gta aca att cat gga atc ctt ggc tgg acc act cct cag 288
 Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
 85 90 95

atg tcc aca aca gct cca aaa atg aag aca aat ata act aat aga tag 336
 Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg *
 100 105 110

<210> 122

<211> 111

<212> PRT

<213> Homo sapiens

<400> 122

Met Lys Leu Leu Leu Leu Leu Leu Thr Val Thr Leu Leu Leu Ala Gln
 1 5 10 15
 Val Thr Pro Gly Leu Pro Ala Met Lys Leu Leu Tyr Leu Phe Leu Ala
 20 25 30
 Ile Leu Leu Ala Ile Glu Glu Pro Val Ile Ser Val Glu Cys Trp Met
 35 40 45
 Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
 50 55 60
 Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
 65 70 75 80
 Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
 85 90 95
 Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg
 100 105 110

<210> 123

<211> 297

<212> DNA

<213> Homo sapiens

<220>

<222> (1) ... (297)

atg cca gag agc ttc ctg ttg gga ctg gga tgg ctg gag ggc atc aca 48
Met Pro Glu Ser Phe Leu Leu Gly Leu Gly Trp Leu Glu Gly Ile Thr
1 5 10 15

gca ctg gtt tcg aac act gaa cgg aga act gcc atg caa caa gaa cct 96
Ala Leu Val Ser Asn Thr Glu Arg Arg Thr Ala Met Gln Gln Glu Pro
20 25 30

ggg cac atc aga ccc ctg cag gca ccc tcg gga ccc aca gat cgc aca 144
Gly His Ile Arg Pro Leu Gln Ala Pro Ser Gly Pro Thr Asp Arg Thr
 35 40 45

ctc gat ggg cgc tcg cag gac gtg aat ggc atc tcg gta acg cca agc 192
Leu Asp Gly Arg Ser Gln Asp Val Asn Gly Ile Ser Val Thr Pro Ser
50 55 60

tcc acc cca gag cca cag gca ggc ggc aac agg gac aag cag acg aca 240
Ser Thr Pro Glu Pro Gln Ala Gly Gly Asn Arg Asp Lys Gln Thr Thr
65 70 75 80

cac ctg ggg cca gag gac gac gca gag aga ccc aca tca gag acc ctc 288
His Leu Gly Pro Glu Asp Asp Ala Glu Arg Pro Thr Ser Glu Thr Leu
85 90 95

gag gag tga 297
Glu Glu *

<211> 98

<212> PRT

$\langle 213 \rangle$ Hom

<213> Homo sapiens

<400> 124

Met Pro Glu Ser Phe Leu Leu Gly Leu Gly Trp Leu Glu Gly Ile Thr
1 5 10 15
Ala Leu Val Ser Asn Thr Glu Arg Arg Thr Ala Met Gln Gln Glu Pro
20 25 30

Gly His Ile Arg Pro Leu Gln Ala Pro Ser Gly Pro Thr Asp Arg Thr
 35 40 45
 Leu Asp Gly Arg Ser Gln Asp Val Asn Gly Ile Ser Val Thr Pro Ser
 50 55 60
 Ser Thr Pro Glu Pro Gln Ala Gly Gly Asn Arg Asp Lys Gln Thr Thr
 65 70 75 80
 His Leu Gly Pro Glu Asp Asp Ala Glu Arg Pro Thr Ser Glu Thr Leu
 85 90 95
 Glu Glu

<210> 125
 <211> 630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(630)

<400> 125
 atg aga tcc ggg agg cac ccc tcg ctg ctg ctg ctt cta gtg ctg ctg 48
 Met Arg Ser Gly Arg His Pro Ser Leu Leu Leu Leu Val Leu Leu
 1 5 10 15
 ctg tgg ctg ctg cag aca ctg ctc act aga tta ggg ccc act cta acc 96
 Leu Trp Leu Leu Gln Thr Leu Leu Thr Arg Leu Gly Pro Thr Leu Thr
 20 25 30
 cag tgt gac ttc atc tta act gta att cag tta aga att aca tct gca 144
 Gln Cys Asp Phe Ile Leu Thr Val Ile Gln Leu Arg Ile Thr Ser Ala
 35 40 45
 aat agc cta ttt cca aat aag gtc ccg ttc aca ggt aaa ccc aac ggg 192
 Asn Ser Leu Phe Pro Asn Lys Val Pro Phe Thr Gly Lys Pro Asn Gly
 50 55 60
 gtc cat gcg cag tcc tat acg atc tta gta ctc ctc atc gcg tcc cga 240
 Val His Ala Gln Ser Tyr Thr Ile Leu Val Leu Leu Ile Ala Ser Arg
 65 70 75 80
 ggt aat gtt tgc agc tgc gta gag tct atc ttt ata ggc cgg ccg atg 288
 Gly Asn Val Cys Ser Cys Val Glu Ser Ile Phe Ile Gly Arg Pro Met

Leu Trp Leu Leu Gln Thr Leu Leu Thr Arg Leu Gly Pro Thr Leu Thr
 20 25 30
 Gln Cys Asp Phe Ile Leu Thr Val Ile Gln Leu Arg Ile Thr Ser Ala
 35 40 45
 Asn Ser Leu Phe Pro Asn Lys Val Pro Phe Thr Gly Lys Pro Asn Gly
 50 55 60
 Val His Ala Gln Ser Tyr Thr Ile Leu Val Leu Leu Ile Ala Ser Arg
 65 70 75 80
 Gly Asn Val Cys Ser Cys Val Glu Ser Ile Phe Ile Gly Arg Pro Met
 85 90 95
 Val Ala Gly Ala Pro Arg Arg Gly Cys Ala His Arg Ala Thr Arg Ile
 100 105 110
 Lys Thr Thr Ile Ile Arg Arg Asn Lys Thr Leu Glu Val Val Gly Leu
 115 120 125
 Lys Leu Phe Leu Leu Val Ser Thr Ala Asp Ser Val Pro Arg Asn Val
 130 135 140
 Arg Ala Val Ser Glu Glu Asp Ala Glu Glu Ser Ser Ala Gly Ser Leu
 145 150 155 160
 Val His Val Phe Gln Lys Phe Ala Asn Ile Pro Val Val Gly Lys Tyr
 165 170 175
 Pro Cys Tyr Phe Gly Glu Ala Leu Pro Arg Leu Ser Arg Leu Asp Tyr
 180 185 190
 Arg Ile Tyr Arg Tyr Cys Ser Gly Cys Gln Arg Leu Arg Cys Cys Gly
 195 200 205
 Glu

<210> 127

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(348)

<400> 127

atg ggg ccc ctt atc tcc ccc ggc act ttc ccc tac atc cgg ctg caa
 Met Gly Pro Leu Ile Ser Pro Gly Thr Phe Pro Tyr Ile Arg Leu Gln
 1 5 10 15

48

cta gaa gct ttc gca cta acc ctc gtg gct gcc cca cgc tgg gcc ctg
 Leu Glu Ala Phe Ala Leu Thr Leu Val Ala Ala Pro Arg Trp Ala Leu

96

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989900

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<210> 128
<211> 115
<212> PRT
<213> Homo sapiens
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<400> 128															
Met	Gly	Pro	Leu	Ile	Ser	Pro	Gly	Thr	Phe	Pro	Tyr	Ile	Arg	Leu	Gln
1				5					10					15	
Leu	Glu	Ala	Phe	Ala	Leu	Thr	Leu	Val	Ala	Ala	Pro	Arg	Trp	Ala	Leu
			20					25					30		
Ala	Phe	Val	Asn	Gly	Ser	Phe	Ile	Lys	Leu	Ser	Pro	Asn	Thr	His	Gly
		35					40					45			
Met	Arg	Val	Thr	Ala	Asp	Ser	Phe	Leu	Pro	Val	Thr	Pro	Ala	Met	Cys
	50					55					60				
Thr	Lys	Ser	Ile	Ser	Asp	Pro	Leu	Leu	Thr	Pro	Pro	Asp	Pro	Val	Lys
65					70					75					80

Lys Ala Ser Met Asn Ala Thr Leu His Ala Gly Val Ser Gly Pro Ala
 85 90 95
 Arg Ser Gln Leu Ser Gly Phe Glu Gly Thr Asp Gly Pro Gly Val Trp
 100 105 110
 Gln Cys Glu
 115

<210> 129

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(660)

<400> 129

atg ggc tca ttg gct tct gag gag aga tac tgg gat gtc tcg gcc ttg 48
 Met Gly Ser Leu Ala Ser Glu Glu Arg Tyr Trp Asp Val Ser Ala Leu
 1 5 10 15

ctg atg gca tta ccc ctt cca gct gcc tct ctc cag aat gat ctc aac 96
 Leu Met Ala Leu Pro Leu Pro Ala Ala Ser Leu Gln Asn Asp Leu Asn
 20 25 30

cag ggt ggc cca ggg agc act aat tcc aag agg cag gcc aac tgg tcc 144
 Gln Gly Gly Pro Gly Ser Thr Asn Ser Lys Arg Gln Ala Asn Trp Ser
 35 40 45

ttg gag gag gag aag agc aga ctg ctg gct gag gca gca ctt gag ttg 192
 Leu Glu Glu Glu Lys Ser Arg Leu Leu Ala Glu Ala Ala Leu Glu Leu
 50 55 60

cgg gag gag aac acg agg cag gaa cgg att ctg gcc ctg gcc aag cga 240
 Arg Glu Glu Asn Thr Arg Gln Glu Arg Ile Leu Ala Leu Ala Lys Arg
 65 70 75 80

cta gcc atg ctg cgg gga cag gac ccc gag aga gtg acc ctc cag gac 288
 Leu Ala Met Leu Arg Gly Gln Asp Pro Glu Arg Val Thr Leu Gln Asp
 85 90 95

tat cgc ctc cca gac agt gat gac gac gag gat gag gag aca gcc atc 336
 Tyr Arg Leu Pro Asp Ser Asp Asp Asp Glu Asp Glu Glu Thr Ala Ile

100	105	110	
caa aga gtc ctg cag cag ctc act gaa gaa gct tcc ctg gat gag gca			384
Gln Arg Val Leu Gln Gln Leu Thr Glu Glu Ala Ser Leu Asp Glu Ala			
115	120	125	
agt ggc ttt aac atc cct gca gag cag gct tct cga ccc tgg acg caa			432
Ser Gly Phe Asn Ile Pro Ala Glu Gln Ala Ser Arg Pro Trp Thr Gln			
130	135	140	
ccc cgc ggg gca gag cct gag gcc cag gat gtg gac ccc agg cct gag			480
Pro Arg Gly Ala Glu Pro Glu Ala Gln Asp Val Asp Pro Arg Pro Glu			
145	150	155	160
gct gag gaa gag gag ctc ccc tgg tgc tgc atc tgc aat gag gat gcc			528
Ala Glu Glu Glu Glu Leu Pro Trp Cys Cys Ile Cys Asn Glu Asp Ala			
165	170	175	
acc cta cgc tgc gct ggc tgc gat ggg gac ctc ttc tgt gcc cgc tgc			576
Thr Leu Arg Cys Ala Gly Cys Asp Gly Asp Leu Phe Cys Ala Arg Cys			
180	185	190	
ttc cga gag ggc cat gat gcc ttt gag ctt aaa gag cac cag aca tct			624
Phe Arg Glu Gly His Asp Ala Phe Glu Leu Lys Glu His Gln Thr Ser			
195	200	205	
gcc tac tct cct cca cgt gca ggc caa gag cac tga			660
Ala Tyr Ser Pro Pro Arg Ala Gly Gln Glu His *			
210	215		

<210> 130

<211> 219

<212> PRT

<213> Homo sapiens

<400> 130

Met Gly Ser Leu Ala Ser Glu Glu Arg Tyr Trp Asp Val Ser Ala Leu			
1	5	10	15
Leu Met Ala Leu Pro Leu Pro Ala Ala Ser Leu Gln Asn Asp Leu Asn			
20	25	30	
Gln Gly Gly Pro Gly Ser Thr Asn Ser Lys Arg Gln Ala Asn Trp Ser			
35	40	45	

Leu Glu Glu Glu Lys Ser Arg Leu Leu Ala Glu Ala Ala Leu Glu Leu
 50 55 60
 Arg Glu Glu Asn Thr Arg Gln Glu Arg Ile Leu Ala Leu Ala Lys Arg
 65 70 75 80
 Leu Ala Met Leu Arg Gly Gln Asp Pro Glu Arg Val Thr Leu Gln Asp
 85 90 95
 Tyr Arg Leu Pro Asp Ser Asp Asp Asp Glu Asp Glu Glu Thr Ala Ile
 100 105 110
 Gln Arg Val Leu Gln Gln Leu Thr Glu Glu Ala Ser Leu Asp Glu Ala
 115 120 125
 Ser Gly Phe Asn Ile Pro Ala Glu Gln Ala Ser Arg Pro Trp Thr Gln
 130 135 140
 Pro Arg Gly Ala Glu Pro Glu Ala Gln Asp Val Asp Pro Arg Pro Glu
 145 150 155 160
 Ala Glu Glu Glu Glu Leu Pro Trp Cys Cys Ile Cys Asn Glu Asp Ala
 165 170 175
 Thr Leu Arg Cys Ala Gly Cys Asp Gly Asp Leu Phe Cys Ala Arg Cys
 180 185 190
 Phe Arg Glu Gly His Asp Ala Phe Glu Leu Lys Glu His Gln Thr Ser
 195 200 205
 Ala Tyr Ser Pro Pro Arg Ala Gly Gln Glu His
 210 215

<210> 131
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(252)

<400> 131

atg cag tgg ctt gct ctg ctt ctc cca cat gca ggc cta gcc cag gca 48
 Met Gln Trp Leu Ala Leu Leu Leu Pro His Ala Gly Leu Ala Gln Ala
 1 5 10 15

atg ctg ctg ggc agg tca gag acc tcc aca cct gtc ctc ttc gcg tgc 96
 Met Leu Leu Gly Arg Ser Glu Thr Ser Thr Pro Val Leu Phe Ala Cys
 20 25 30

cac atg gac acg ggc ctg cgc agc gtg gcc aac atc tgg ttc caa tgt 144
 His Met Asp Thr Gly Leu Arg Ser Val Ala Asn Ile Trp Phe Gln Cys

35	40	45	
gtg gtt ccc atg cca ctg gct gac tac ccc aat gat gac atg gcc cac	192		
Val Val Pro Met Pro Leu Ala Asp Tyr Pro Asn Asp Asp Met Ala His			
50 55 60			
gtt gtc ccc acg gag tcg ctg ctg ctc tca gcc acc gtc acg cgg aga	240		
Val Val Pro Thr Glu Ser Leu Leu Leu Ser Ala Thr Val Thr Arg Arg			
65 70 75 80			
gac agg tcc tga	252		
Asp Arg Ser *			

<210> 132
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 132

Met Gln Trp Leu Ala Leu Leu Leu Pro His Ala Gly Leu Ala Gln Ala	
1 5 10 15	
Met Leu Leu Gly Arg Ser Glu Thr Ser Thr Pro Val Leu Phe Ala Cys	
20 25 30	
His Met Asp Thr Gly Leu Arg Ser Val Ala Asn Ile Trp Phe Gln Cys	
35 40 45	
Val Val Pro Met Pro Leu Ala Asp Tyr Pro Asn Asp Asp Met Ala His	
50 55 60	
Val Val Pro Thr Glu Ser Leu Leu Leu Ser Ala Thr Val Thr Arg Arg	
65 70 75 80	
Asp Arg Ser	

<210> 133
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(378)

Met Ala Lys Ile Gly Glu Glu Ser Leu Asn Cys Thr Pro Ser Asp Ala
1 5 10 15
Leu Gln Tyr Lys Gly Met Phe Leu Met Tyr Leu Leu Pro Gly Val Phe

20 25 30
 Gly Gln Val Arg Cys Pro Ile Pro Pro Gln Asp Ser Lys Arg Lys Val
 35 40 45
 Arg Ser Lys His Pro Ala Arg Lys Ile Ser Arg Arg Asp Thr Arg Thr
 50 55 60
 His Arg Leu Leu Leu Asn Arg Ala Ser Pro Trp Pro Ile Ser Pro His
 65 70 75 80
 Ala Glu Thr Asn Arg Lys Ala Ala Leu Ala Gln Ile Ala His Tyr Pro
 85 90 95
 Lys Pro Pro Thr Ser Trp Asn Ala Glu Ala Asp Asp Asn Ser Gln Gly
 100 105 110
 Thr Arg Ile Arg Asp Gln Ala Ala Pro His Arg Leu Phe
 115 120 125

<210> 135
 <211> 87
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(87)

<400> 135

atg agc tgg cca cac aaa ctg ctg ctg ctg ctg ctt cta ggt ggc tgc 48
 Met Ser Trp Pro His Lys Leu Leu Leu Leu Leu Leu Gly Gly Cys
 1 5 10 15

ctt gct ggt ata ctt act ccc tac ttc atg aac tca tga 87
 Leu Ala Gly Ile Leu Thr Pro Tyr Phe Met Asn Ser *
 20 25

<210> 136
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 136

Met Ser Trp Pro His Lys Leu Leu Leu Leu Leu Leu Gly Gly Cys
 1 5 10 15
 Leu Ala Gly Ile Leu Thr Pro Tyr Phe Met Asn Ser
 20 25

<210> 137
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(558)

<400> 137

atg ggg ctt gat gaa cag ctt ttt ggg gca cta gaa gcc tcc tgg ggt	48
Met Gly Leu Asp Glu Gln Leu Phe Gly Ala Leu Glu Ala Ser Trp Gly	
1 5 10 15	
acc tgt cat gcc ctt gaa cgt ttc ttg gag cgt gcc ttt ttc cac cct	96
Thr Cys His Ala Leu Glu Arg Phe Leu Glu Arg Ala Phe Phe His Pro	
20 25 30	
gcc atg aag ccc gaa gtt ctt cta ttg gca acc aaa ttt cca ctg tcc	144
Ala Met Lys Pro Glu Val Leu Leu Leu Ala Thr Lys Phe Pro Leu Ser	
35 40 45	
ctg ggc aaa aga aaa ggg ccc tca tgt gcg ctt aga aga tct ggc gag	192
Leu Gly Lys Arg Lys Gly Pro Ser Cys Ala Leu Arg Arg Ser Gly Glu	
50 55 60	
gac gaa att tat cat gta acc aga aac cta cag aat ttg ctt ttc ata	240
Asp Glu Ile Tyr His Val Thr Arg Asn Leu Gln Asn Leu Leu Phe Ile	
65 70 75 80	
gga aag tca gcc aaa aat atc aac agc cac aat tta tca gac gcc ttc	288
Gly Lys Ser Ala Lys Asn Ile Asn Ser His Asn Leu Ser Asp Ala Phe	
85 90 95	
agg aaa aat gtc aaa gcc agg cat ttg tct gaa gtg acc tat cct gct	336
Arg Lys Asn Val Lys Ala Arg His Leu Ser Glu Val Thr Tyr Pro Ala	
100 105 110	
tca gaa gtc tat cag cca ttt cca ttc ctg ctt ctg aat gga atc aat	384
Ser Glu Val Tyr Gln Pro Phe Pro Phe Leu Leu Leu Asn Gly Ile Asn	
115 120 125	

cag aaa cat ttc cag ccc cca ctt ctg gta acc gac cag aat agc tgc 432
 Gln Lys His Phe Gln Pro Pro Leu Leu Val Thr Asp Gln Asn Ser Cys
 130 135 140

gga cta agg gtt gcc tta cca ccc cct gct ccg acg tct agc agg aat 480
 Gly Leu Arg Val Ala Leu Pro Pro Pro Ala Pro Thr Ser Ser Arg Asn
 145 150 155 160

cca cca gat gca ctg aga ctc ctg tct caa aaa cat aac caa aat aac 528
 Pro Pro Asp Ala Leu Arg Leu Leu Ser Gln Lys His Asn Gln Asn Asn
 165 170 175

ccc aac ggc att aca ata aat ata caa taa 558
 Pro Asn Gly Ile Thr Ile Asn Ile Gln *
 180 185

<210> 138

<211> 185

<212> PRT

<213> Homo sapiens

<400> 138

Met Gly Leu Asp Glu Gln Leu Phe Gly Ala Leu Glu Ala Ser Trp Gly
 1 5 10 15
 Thr Cys His Ala Leu Glu Arg Phe Leu Glu Arg Ala Phe Phe His Pro
 20 25 30
 Ala Met Lys Pro Glu Val Leu Leu Leu Ala Thr Lys Phe Pro Leu Ser
 35 40 45
 Leu Gly Lys Arg Lys Gly Pro Ser Cys Ala Leu Arg Arg Ser Gly Glu
 50 55 60
 Asp Glu Ile Tyr His Val Thr Arg Asn Leu Gln Asn Leu Leu Phe Ile
 65 70 75 80
 Gly Lys Ser Ala Lys Asn Ile Asn Ser His Asn Leu Ser Asp Ala Phe
 85 90 95
 Arg Lys Asn Val Lys Ala Arg His Leu Ser Glu Val Thr Tyr Pro Ala
 100 105 110
 Ser Glu Val Tyr Gln Pro Phe Pro Phe Leu Leu Leu Asn Gly Ile Asn
 115 120 125
 Gln Lys His Phe Gln Pro Pro Leu Leu Val Thr Asp Gln Asn Ser Cys
 130 135 140
 Gly Leu Arg Val Ala Leu Pro Pro Pro Ala Pro Thr Ser Ser Arg Asn
 145 150 155 160

Pro Pro Asp Ala Leu Arg Leu Leu Ser Gln Lys His Asn Gln Asn Asn
 165 170 175
 Pro Asn Gly Ile Thr Ile Asn Ile Gln
 180 185

<210> 139
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(303)

<400> 139

atg acc aga gca cct ctc ctg cta cta tgt gtt gcc ctg gtg ctg ctt	48
Met Thr Arg Ala Pro Leu Leu Leu Leu Cys Val Ala Leu Val Leu Leu	
1 5 10 15	
ggg cat gtg aat gga gcc aca gta aga aat gag gac aaa tgg aag cca	96
Gly His Val Asn Gly Ala Thr Val Arg Asn Glu Asp Lys Trp Lys Pro	
20 25 30	
ctc aac aac ccc aga aac aga gat ctg ttt ttc aga agg ctt cag gca	144
Leu Asn Asn Pro Arg Asn Arg Asp Leu Phe Phe Arg Arg Leu Gln Ala	
35 40 45	
tat ttt aag ggc aga ggt ctt gat ctt gga aca ttt cca aat cct ttc	192
Tyr Phe Lys Gly Arg Gly Leu Asp Leu Gly Thr Phe Pro Asn Pro Phe	
50 55 60	
ccc acg aat gaa aat cct aga cct ctc tct ttc cag tca gaa ctt act	240
Pro Thr Asn Glu Asn Pro Arg Pro Leu Ser Phe Gln Ser Glu Leu Thr	
65 70 75 80	
gct tct gca tct gca gat tat gaa gag cag aaa aac tcc ttt cac aat	288
Ala Ser Ala Ser Ala Asp Tyr Glu Glu Gln Lys Asn Ser Phe His Asn	
85 90 95	
tat ctc aaa ggc tga	303
Tyr Leu Lys Gly *	
100	

<210> 140
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 140

Met Thr Arg Ala Pro Leu Leu Leu Leu Cys Val Ala Leu Val Leu Leu
 1 5 10 15
 Gly His Val Asn Gly Ala Thr Val Arg Asn Glu Asp Lys Trp Lys Pro
 20 25 30
 Leu Asn Asn Pro Arg Asn Arg Asp Leu Phe Phe Arg Arg Leu Gln Ala
 35 40 45
 Tyr Phe Lys Gly Arg Gly Leu Asp Leu Gly Thr Phe Pro Asn Pro Phe
 50 55 60
 Pro Thr Asn Glu Asn Pro Arg Pro Leu Ser Phe Gln Ser Glu Leu Thr
 65 70 75 80
 Ala Ser Ala Ser Ala Asp Tyr Glu Glu Gln Lys Asn Ser Phe His Asn
 85 90 95
 Tyr Leu Lys Gly
 100

<210> 141
 <211> 687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(687)

<400> 141

atg cgg ccc ctt aag ccc ggc gcc cct ttg ccc gca ctc ttc ctg ctg 48
 Met Arg Pro Leu Lys Pro Gly Ala Pro Leu Pro Ala Leu Phe Leu Leu
 1 5 10 15
 gcg ctg gct ttg tcc ccg cac gga gcc cac ggg agg ccc cgg ggg cgc 96
 Ala Leu Ala Leu Ser Pro His Gly Ala His Gly Arg Pro Arg Gly Arg
 20 25 30
 agg gga gcg cgc gtc acg gat aag gag ccc aag ccg ttg ctt ttc ctc 144
 Arg Gly Ala Arg Val Thr Asp Lys Glu Pro Lys Pro Leu Leu Phe Leu
 35 40 45

ccc gcg gcc ggg gcc ggc cgg act ccc agc ggc tcc cgg agc gca gga	192
Pro Ala Ala Gly Ala Gly Arg Thr Pro Ser Gly Ser Arg Ser Ala Gly	
50 55 60	
 gct ggg cga ggc act cgc ttt ggg aag cct gag att agt aca gca gaa	240
Ala Gly Arg Gly Thr Arg Phe Gly Lys Pro Glu Ile Ser Thr Ala Glu	
65 70 75 80	
 aac aga gca tct ctg cag att ccc agc tct cgg aaa gag gtc agg gtc	288
Asn Arg Ala Ser Leu Gln Ile Pro Ser Ser Arg Lys Glu Val Arg Val	
85 90 95	
 atg aga cat cca cag gca gag aag tcg tgt gaa tac ggg gaa cac gga	336
Met Arg His Pro Gln Ala Glu Lys Ser Cys Glu Tyr Gly Glu His Gly	
100 105 110	
 aaa gcc ccg gaa aag gag gtc cga ggg ggc ggc ccg ggc act tgg ggc	384
Lys Ala Pro Glu Lys Glu Val Arg Gly Gly Gly Pro Gly Thr Trp Gly	
115 120 125	
 agc gct gga ggg agg agg gca gga cac gca gga aag gaa ggt ggg gac	432
Ser Ala Gly Gly Arg Arg Ala Gly His Ala Gly Lys Glu Gly Gly Asp	
130 135 140	
 aga agc gag aag ctc ctc aca cgt ttc tgt tca cac cca gca aga gca	480
Arg Ser Glu Lys Leu Leu Thr Arg Phe Cys Ser His Pro Ala Arg Ala	
145 150 155 160	
 gag caa ggt gaa gct gcc ggc gag gct ggg aca gaa ggg ccc ctc tgc	528
Glu Gln Gly Glu Ala Ala Gly Glu Ala Gly Thr Glu Gly Pro Leu Cys	
165 170 175	
 ggg gac att tgg tgg cct cca ccg ggc ttg gga aga gga gag ggc cta	576
Gly Asp Ile Trp Trp Pro Pro Pro Gly Leu Gly Arg Gly Glu Gly Leu	
180 185 190	
 ggg tgg cct ggg gat gcc tcg cag cta gcg gct ggc cgt ggg acc aca	624
Gly Trp Pro Gly Asp Ala Ser Gln Leu Ala Ala Gly Arg Gly Thr Thr	
195 200 205	
 gct cct gat ccc ttc tcc tca ggc ttt atg gct aag aaa gca aac aag	672
Ala Pro Asp Pro Phe Ser Ser Gly Phe Met Ala Lys Lys Ala Asn Lys	

[illegible]

<210> 143
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(393)

<400> 143

atg ggg ttt ctc cat gtt gag gct ggt ctc gta ctc ctg acc tca ggc	48
Met Gly Phe Leu His Val Glu Ala Gly Leu Val Leu Leu Thr Ser Gly	
1 5 10 15	
gtg gtc ccg ctc gca cga ggg agc ggt cgc cca ggg tgc cgg gaa gtc	96
Val Val Pro Leu Ala Arg Gly Ser Gly Arg Pro Gly Cys Arg Glu Val	
20 25 30	
ggg gac cgg cca gcc gcc gac cgg ccg cac ccc tcc ccg ccg agc tcg	144
Gly Asp Arg Pro Ala Ala Asp Arg Pro His Pro Ser Pro Pro Ser Ser	
35 40 45	
cgc gcc cgc ctc gtc agc acc ttt ccc gca gcg cag ccc cac agt ggt	192
Arg Ala Arg Leu Val Ser Thr Phe Pro Ala Ala Gln Pro His Ser Gly	
50 55 60	
cac gag agc cgc ggc ccg aaa aga cgc gaa ggt ggt gac gtg tcc cgt	240
His Glu Ser Arg Gly Pro Lys Arg Arg Glu Gly Gly Asp Val Ser Arg	
65 70 75 80	
gcc cag ggc gct gcg cag gag gca ttg gca act gac gtc ctg cgc gcc	288
Ala Gln Gly Ala Ala Gln Glu Ala Leu Ala Thr Asp Val Leu Arg Ala	
85 90 95	
gcc tgg tgg aag caa agc agc cga gcc ccc cgg aag cgg cgg cgc ggg	336
Ala Trp Trp Lys Gln Ser Ser Arg Ala Pro Arg Lys Arg Arg Arg Gly	
100 105 110	
cga gtg gag aac gtg act tac gtc atc tgg cgg agg cgt ggg ggc ggt	384
Arg Val Glu Asn Val Thr Tyr Val Ile Trp Arg Arg Arg Gly Gly Gly	
115 120 125	

gcc gcg tga
Ala Ala *
130

393

<210> 144
<211> 130
<212> PRT
<213> Homo sapiens

<400> 144

Met Gly Phe Leu His Val Glu Ala Gly Leu Val Leu Leu Thr Ser Gly
1 5 10 15
Val Val Pro Leu Ala Arg Gly Ser Gly Arg Pro Gly Cys Arg Glu Val
20 25 30
Gly Asp Arg Pro Ala Ala Asp Arg Pro His Pro Ser Pro Pro Ser Ser
35 40 45
Arg Ala Arg Leu Val Ser Thr Phe Pro Ala Ala Gln Pro His Ser Gly
50 55 60
His Glu Ser Arg Gly Pro Lys Arg Arg Glu Gly Gly Asp Val Ser Arg
65 70 75 80
Ala Gln Gly Ala Ala Gln Glu Ala Leu Ala Thr Asp Val Leu Arg Ala
85 90 95
Ala Trp Trp Lys Gln Ser Ser Arg Ala Pro Arg Lys Arg Arg Arg Gly
100 105 110
Arg Val Glu Asn Val Thr Tyr Val Ile Trp Arg Arg Arg Gly Gly Gly
115 120 125
Ala Ala
130

<210> 145
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(666)

<400> 145

atg gat acc agc acc tgc tct ggt gga agt ggg agg gga gta aag tgg
Met Asp Thr Ser Thr Cys Ser Gly Gly Ser Gly Arg Gly Val Lys Trp
1 5 10 15

48

act	ctg	cgg	gag	tcc	ttg	gtt	tta	gtt	ttg	ttt	agt	gca	ctg	gtt	ttc	96
Thr	Leu	Arg	Glu	Ser	Leu	Val	Leu	Val	Leu	Phe	Ser	Ala	Leu	Val	Phe	
			20					25					30			
tca	aat	gct	ggg	tat	gct	agc	tgt	gaa	gct	gtc	aca	cag	aca	gac	tca	144
Ser	Asn	Ala	Gly	Tyr	Ala	Ser	Cys	Glu	Ala	Val	Thr	Gln	Thr	Asp	Ser	
		35					40					45				
cga	cct	ctg	gtt	agc	cag	ggg	gtt	gca	gga	ttt	tca	ggg	tcc	cag	tgg	192
Arg	Pro	Leu	Val	Ser	Gln	Gly	Val	Ala	Gly	Phe	Ser	Gly	Ser	Gln	Trp	
	50					55					60					
gat	gtg	ggg	gca	gag	gca	gac	ttc	tcc	tcc	tct	cac	acc	ttg	gga	act	240
Asp	Val	Gly	Ala	Glu	Ala	Asp	Phe	Ser	Ser	Ser	His	Thr	Leu	Gly	Thr	
	65				70					75					80	
cac	gta	gag	ttt	gca	gcg	gta	agc	tgc	ttc	ttt	caa	agg	gtc	tgt	gaa	288
His	Val	Glu	Phe	Ala	Ala	Val	Ser	Cys	Phe	Phe	Gln	Arg	Val	Cys	Glu	
				85					90					95		
ttc	ttt	cag	ttt	tcc	tgg	tat	gtt	cct	gtg	gtg	gtt	ctt	gga	gca	aaa	336
Phe	Phe	Gln	Phe	Ser	Trp	Tyr	Val	Pro	Val	Val	Val	Leu	Gly	Ala	Lys	
			100					105					110			
ctt	cac	aat	cta	gaa	gag	aaa	ggc	gag	gaa	tgg	cac	tgc	ctt	ctg	aaa	384
Leu	His	Asn	Leu	Glu	Glu	Lys	Gly	Glu	Glu	Trp	His	Cys	Leu	Leu	Lys	
		115					120					125				
gat	gac	tgg	ctt	cta	ctt	cct	tct	ctt	gtc	cag	ttc	atg	aac	tcc	ctg	432
Asp	Asp	Trp	Leu	Leu	Leu	Pro	Ser	Leu	Val	Gln	Phe	Met	Asn	Ser	Leu	
		130				135					140					
gag	ttt	tgc	aat	gca	gtc	ata	cag	gtg	gct	cac	ccc	ttg	att	cga	aat	480
Glu	Phe	Cys	Asn	Ala	Val	Ile	Gln	Val	Ala	His	Pro	Leu	Ile	Arg	Asn	
					150				155						160	
cag	ctt	gtc	aat	tac	att	tac	aat	gga	ttt	ttg	gta	cca	gtc	ttg	gct	528
Gln	Leu	Val	Asn	Tyr	Ile	Tyr	Asn	Gly	Phe	Leu	Val	Pro	Val	Leu	Ala	
				165					170					175		
cct	gct	ctc	cat	aag	tgg	caa	ctt	gga	act	gtc	aag	atg	ttc	tcc	aag	576
Pro	Ala	Leu	His	Lys	Trp	Gln	Leu	Gly	Thr	Val	Lys	Met	Phe	Ser	Lys	

<210> 146
<211> 221
<212> PRT
<213> Homo sapiens

<400> 146																
Met	Asp	Thr	Ser	Thr	Cys	Ser	Gly	Gly	Ser	Gly	Arg	Gly	Val	Lys	Trp	
1				5					10					15		
Thr	Leu	Arg	Glu	Ser	Leu	Val	Leu	Val	Leu	Phe	Ser	Ala	Leu	Val	Phe	
			20					25					30			
Ser	Asn	Ala	Gly	Tyr	Ala	Ser	Cys	Glu	Ala	Val	Thr	Gln	Thr	Asp	Ser	
		35					40					45				
Arg	Pro	Leu	Val	Ser	Gln	Gly	Val	Ala	Gly	Phe	Ser	Gly	Ser	Gln	Trp	
	50					55					60					
Asp	Val	Gly	Ala	Glu	Ala	Asp	Phe	Ser	Ser	Ser	His	Thr	Leu	Gly	Thr	
65				70						75					80	
His	Val	Glu	Phe	Ala	Ala	Val	Ser	Cys	Phe	Phe	Gln	Arg	Val	Cys	Glu	
			85						90					95		
Phe	Phe	Gln	Phe	Ser	Trp	Tyr	Val	Pro	Val	Val	Val	Leu	Gly	Ala	Lys	
			100					105					110			
Leu	His	Asn	Leu	Glu	Glu	Lys	Gly	Glu	Glu	Trp	His	Cys	Leu	Leu	Lys	
		115					120					125				
Asp	Asp	Trp	Leu	Leu	Leu	Pro	Ser	Leu	Val	Gln	Phe	Met	Asn	Ser	Leu	
	130					135					140					
Glu	Phe	Cys	Asn	Ala	Val	Ile	Gln	Val	Ala	His	Pro	Leu	Ile	Arg	Asn	
145				150						155					160	
Gln	Leu	Val	Asn	Tyr	Ile	Tyr	Asn	Gly	Phe	Leu	Val	Pro	Val	Leu	Ala	
			165						170					175		
Pro	Ala	Leu	His	Lys	Trp	Gln	Leu	Gly	Thr	Val	Lys	Met	Phe	Ser	Lys	
			180					185				190				
Ala	Glu	Ser	Val	Ile	Glu	Asn	Ala	Arg	Ser	Ala	Val	Gly	Met	Glu	Arg	
		195					200					205				

Ser Ser Gly Ser Thr Ser Ala Ile Asp Leu Pro Ser Thr
 210 215 220

<210> 147
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(438)

<400> 147

atg gct cgg gca ggg ggc atg ggg ctg ctg cga tta cag ctg ctt ctg	48
Met Ala Arg Ala Gly Gly Met Gly Leu Leu Arg Leu Gln Leu Leu Leu	
1 5 10 15	
gta ctg ccc aca cta gct tct gcc tgt gtg ccc tgc atc tac ctg gtt	96
Val Leu Pro Thr Leu Ala Ser Ala Cys Val Pro Cys Ile Tyr Leu Val	
20 25 30	
ccc acg tgg acg tcc cta tct gag aca cct ttt gga cca act ctg gac	144
Pro Thr Trp Thr Ser Leu Ser Glu Thr Pro Phe Gly Pro Thr Leu Asp	
35 40 45	
aga ccc tct cca aaa tca aag gtg cgc tgg gct gct aac ctg atc caa	192
Arg Pro Ser Pro Lys Ser Lys Val Arg Trp Ala Ala Asn Leu Ile Gln	
50 55 60	
gac gag atc aat cta gaa gga cct gct ggt gct gca acc cac gct tgg	240
Asp Glu Ile Asn Leu Glu Gly Pro Ala Gly Ala Ala Thr His Ala Trp	
65 70 75 80	
gtc acc ttt gcc aga acc ggg gtc att tgc ttt ggg ggt cct cag gcc	288
Val Thr Phe Ala Arg Thr Gly Val Ile Cys Phe Gly Gly Pro Gln Ala	
85 90 95	
agt gct cag aag gct gct tgt tgt aga tgg agg aca gct cct cag gct	336
Ser Ala Gln Lys Ala Ala Cys Cys Arg Trp Arg Thr Ala Pro Gln Ala	
100 105 110	
ggg aaa tct ctc aat ggg aac tgt gct cag aac aga aca gaa ctt ccc	384
Gly Lys Ser Leu Asn Gly Asn Cys Ala Gln Asn Arg Thr Glu Leu Pro	

115 120 125

gga tac tta gat att tgg gtg gta ttg atc tcc gca tca gtg tcc tcg 432
 Gly Tyr Leu Asp Ile Trp Val Val Leu Ile Ser Ala Ser Val Ser Ser
 130 135 140

ggt tga 438
 Gly *
 145

<210> 148
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 148

Met Ala Arg Ala Gly Gly Met Gly Leu Leu Arg Leu Gln Leu Leu Leu
 1 5 10 15
 Val Leu Pro Thr Leu Ala Ser Ala Cys Val Pro Cys Ile Tyr Leu Val
 20 25 30
 Pro Thr Trp Thr Ser Leu Ser Glu Thr Pro Phe Gly Pro Thr Leu Asp
 35 40 45
 Arg Pro Ser Pro Lys Ser Lys Val Arg Trp Ala Ala Asn Leu Ile Gln
 50 55 60
 Asp Glu Ile Asn Leu Glu Gly Pro Ala Gly Ala Ala Thr His Ala Trp
 65 70 75 80
 Val Thr Phe Ala Arg Thr Gly Val Ile Cys Phe Gly Gly Pro Gln Ala
 85 90 95
 Ser Ala Gln Lys Ala Ala Cys Cys Arg Trp Arg Thr Ala Pro Gln Ala
 100 105 110
 Gly Lys Ser Leu Asn Gly Asn Cys Ala Gln Asn Arg Thr Glu Leu Pro
 115 120 125
 Gly Tyr Leu Asp Ile Trp Val Val Leu Ile Ser Ala Ser Val Ser Ser
 130 135 140

Gly
 145

<210> 149
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(411)

<400> 149

atg tgg gtg ctg ctg ctg ctg ttg gag gca ggc ctc ggg gct ctg	48
Met Trp Val Leu Leu Leu Leu Leu Leu Glu Ala Gly Leu Gly Ala Leu	
1 5 10 15	
act ctg gag ggt tgt gaa ttc cag cgg cac ggg gct gtt gtg tgc ctt	96
Thr Leu Glu Gly Cys Glu Phe Gln Arg His Gly Ala Val Val Cys Leu	
20 25 30	
gtt cac ggc cat ctc cct tcc acc cag tgt cta gcc cag tgt ctg tac	144
Val His Gly His Leu Pro Ser Thr Gln Cys Leu Ala Gln Cys Leu Tyr	
35 40 45	
aca gca gat gcg aag cta cgt gac gtt gtc cgt gaa cca gcc ggg ccc	192
Thr Ala Asp Ala Lys Leu Arg Asp Val Val Arg Glu Pro Ala Gly Pro	
50 55 60	
gcg ttg ccc tac tca act atg tcg agg agc ccc ggt cac cag cgg tct	240
Ala Leu Pro Tyr Ser Thr Met Ser Arg Ser Pro Gly His Gln Arg Ser	
65 70 75 80	
gac cca ttt aac aat tct ggc tct acc gat atc cag ttg ctc gcc cgg	288
Asp Pro Phe Asn Asn Ser Gly Ser Thr Asp Ile Gln Leu Leu Ala Arg	
85 90 95	
gtc cac tca ccg aaa atc tct ata tgt aat tct aag cct aaa aag acg	336
Val His Ser Pro Lys Ile Ser Ile Cys Asn Ser Lys Pro Lys Lys Thr	
100 105 110	
ggc acg caa tac cac gac ggc gac ctg ctc acg ttc gtc ccc agc gat	384
Gly Thr Gln Tyr His Asp Gly Asp Leu Leu Thr Phe Val Pro Ser Asp	
115 120 125	
gca ctg ggg gag gca cgt cgg cgg tga	411
Ala Leu Gly Glu Ala Arg Arg *	
130 135	

<210> 150

<211> 136
 <212> PRT
 <213> Homo sapiens

<400> 150

Met Trp Val Leu Leu Leu Leu Leu Leu Glu Ala Gly Leu Gly Ala Leu
 1 5 10 15
 Thr Leu Glu Gly Cys Glu Phe Gln Arg His Gly Ala Val Val Cys Leu
 20 25 30
 Val His Gly His Leu Pro Ser Thr Gln Cys Leu Ala Gln Cys Leu Tyr
 35 40 45
 Thr Ala Asp Ala Lys Leu Arg Asp Val Val Arg Glu Pro Ala Gly Pro
 50 55 60
 Ala Leu Pro Tyr Ser Thr Met Ser Arg Ser Pro Gly His Gln Arg Ser
 65 70 75 80
 Asp Pro Phe Asn Asn Ser Gly Ser Thr Asp Ile Gln Leu Leu Ala Arg
 85 90 95
 Val His Ser Pro Lys Ile Ser Ile Cys Asn Ser Lys Pro Lys Lys Thr
 100 105 110
 Gly Thr Gln Tyr His Asp Gly Asp Leu Leu Thr Phe Val Pro Ser Asp
 115 120 125
 Ala Leu Gly Glu Ala Arg Arg Arg
 130 135

<210> 151
 <211> 852
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(852)

<400> 151

atg gtt tcg gcg gca gcc ccc agc ctc ctc atc ctt ctg ttg ctg ctc 48
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu Leu
 1 5 10 15
 ctg ggg tct gtg cct gct acc gac gcc cgc tct gtg ccc ctg aag gcc 96
 Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu Lys Ala
 20 25 30
 acg ttc ctg gag gat gtg gcg ggt agt ggg gag gcc gag gcc tcg tcg 144

Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser		
35						40						45					
gcc	tcc	tcc	ccg	agc	ctc	ccg	cca	ccc	tgg	acc	ccg	gcc	ctc	agc	ccc	192	
Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	Ala	Leu	Ser	Pro		
50						55						60					
aca	tcg	atg	ggg	ccc	cag	ccc	ata	acc	ctg	ggg	ggc	cca	tca	ccc	ccc	240	
Thr	Ser	Met	Gly	Pro	Gln	Pro	Ile	Thr	Leu	Gly	Gly	Pro	Ser	Pro	Pro		
65						70						75			80		
acc	aac	ttc	ctg	gat	ggg	ata	gtg	gac	ttc	ttc	cgc	cag	tac	gtg	atg	288	
Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met		
			85						90						95		
ctg	att	gct	gtg	gtg	ggc	tcc	ctg	gcc	ttt	ctg	ctg	atg	ttc	atc	gtc	336	
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val		
			100						105						110		
tgt	gcc	gcg	gtc	atc	acc	cgg	cag	aag	cag	aag	gcc	tcg	gcc	tat	tac	384	
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr		
115						120						125					
cca	tcg	tcc	ttc	ccc	aag	aag	aag	tac	gtg	gac	cag	agt	gac	cgg	gcc	432	
Pro	Ser	Ser	Phe	Pro	Lys	Lys	Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala		
130						135						140					
ggg	ggc	ccc	cgg	gcc	ttc	agt	gag	gtc	ccc	gac	aga	gcc	ccc	gac	agc	480	
Gly	Gly	Pro	Arg	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser		
145						150						155			160		
agg	ccc	gag	gaa	gcc	ctg	gat	tcc	tcc	cgg	cag	ctc	cag	gcc	gac	atc	528	
Arg	Pro	Glu	Glu	Ala	Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile		
			165						170						175		
ttg	gcc	gcc	acc	cag	aac	ctc	aag	tcc	ccc	acc	agg	gct	gca	ctg	ggc	576	
Leu	Ala	Ala	Thr	Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly		
			180						185						190		
ggt	ggg	gac	gga	gcc	agg	atg	gtg	gag	ggc	agg	ggc	gca	gag	gaa	gag	624	
Gly	Gly	Asp	Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu		
195						200						205					

Pro Ser Ser Phe Pro Lys Lys Lys Tyr Val Asp Gln Ser Asp Arg Ala
 130 135 140
 Gly Gly Pro Arg Ala Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser
 145 150 155 160
 Arg Pro Glu Glu Ala Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile
 165 170 175
 Leu Ala Ala Thr Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly
 180 185 190
 Gly Gly Asp Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu
 195 200 205
 Glu Lys Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val
 210 215 220
 Pro Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 225 230 235 240
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly Ser
 245 250 255
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270
 Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
 275 280

<210> 153

<211> 696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(696)

<400> 153

atg ggc gag ggc tcc aaa ggg ccc tgc atg tgc tgt tcc cct gcc tgg 48
 Met Gly Glu Gly Ser Lys Gly Pro Cys Met Cys Cys Ser Pro Ala Trp
 1 5 10 15

atg ccc acc ccc aag ggt cac ctc ctc cag gaa gcc ttc ctt ctt ctc 96
 Met Pro Thr Pro Lys Gly His Leu Leu Gln Glu Ala Phe Leu Leu Leu
 20 25 30

agg ctg agt tgg ctg gtt act gct gtg cct gct ctt gac tgg gga ttc 144
 Arg Leu Ser Trp Leu Val Thr Ala Val Pro Ala Leu Asp Trp Gly Phe
 35 40 45

tac cgg ggc gag gcc agg ctg ctc tta tcc atc gtc atg tcc tca gtg	192
Tyr Arg Gly Glu Ala Arg Leu Leu Leu Ser Ile Val Met Ser Ser Val	
50 55 60	
ggc aca cag aga cct gtg acc atc agt cag tgt gac agg ccc ctg gca	240
Gly Thr Gln Arg Pro Val Thr Ile Ser Gln Cys Asp Arg Pro Leu Ala	
65 70 75 80	
acc acc aat cga ctt gtt gtc tcc gtg gct ttg caa ttt ctg aca ttt	288
Thr Thr Asn Arg Leu Val Val Ser Val Ala Leu Gln Phe Leu Thr Phe	
85 90 95	
cat gaa agt gga atc aca agt gcc ctc cgt gtc cgg cct ctt cca cag	336
His Glu Ser Gly Ile Thr Ser Ala Leu Arg Val Arg Pro Leu Pro Gln	
100 105 110	
agc gtt gag ttt tca agg ttc gtc cct gtt gta gca gga atc cgt gct	384
Ser Val Glu Phe Ser Arg Phe Val Pro Val Val Ala Gly Ile Arg Ala	
115 120 125	
tca ctt agg ctg caa ggg cgt acc atg gca tgg agg cac cta tgg gtg	432
Ser Leu Arg Leu Gln Gly Arg Thr Met Ala Trp Arg His Leu Trp Val	
130 135 140	
gac ggc gtt tcg ctg gtc tgt cct ggg ctg agg gct gag ggc tgg aca	480
Asp Gly Val Ser Leu Val Cys Pro Gly Leu Arg Ala Glu Gly Trp Thr	
145 150 155 160	
ccc cca cct ggc tcc cgt gtc ctg ttg aag agg tgt cga atc ttc gcc	528
Pro Pro Pro Gly Ser Arg Val Leu Leu Lys Arg Cys Arg Ile Phe Ala	
165 170 175	
gct ctc gag atg cac gtg tgc agc ttt ggc cga tcc cct gtt ttc agc	576
Ala Leu Glu Met His Val Cys Ser Phe Gly Arg Ser Pro Val Phe Ser	
180 185 190	
tgc aac tgt ctc ccg aag tca cag att ccc cct tgg tct ttg gtg tgc	624
Cys Asn Cys Leu Pro Lys Ser Gln Ile Pro Pro Trp Ser Leu Val Cys	
195 200 205	
ggg gag ggc tac aaa tcc tcc cca aga atg ccc acc ctg ccc ccg act	672
Gly Glu Gly Tyr Lys Ser Ser Pro Arg Met Pro Thr Leu Pro Pro Thr	
210 215 220	

ggg gca gat tct ggt tat cca tag
 Gly Ala Asp Ser Gly Tyr Pro *
 225 230

696

<210> 154
 <211> 231
 <212> PRT
 <213> Homo sapiens

<400> 154

Met Gly Glu Gly Ser Lys Gly Pro Cys Met Cys Cys Ser Pro Ala Trp
 1 5 10 15
 Met Pro Thr Pro Lys Gly His Leu Leu Gln Glu Ala Phe Leu Leu Leu
 20 25 30
 Arg Leu Ser Trp Leu Val Thr Ala Val Pro Ala Leu Asp Trp Gly Phe
 35 40 45
 Tyr Arg Gly Glu Ala Arg Leu Leu Leu Ser Ile Val Met Ser Ser Val
 50 55 60
 Gly Thr Gln Arg Pro Val Thr Ile Ser Gln Cys Asp Arg Pro Leu Ala
 65 70 75 80
 Thr Thr Asn Arg Leu Val Val Ser Val Ala Leu Gln Phe Leu Thr Phe
 85 90 95
 His Glu Ser Gly Ile Thr Ser Ala Leu Arg Val Arg Pro Leu Pro Gln
 100 105 110
 Ser Val Glu Phe Ser Arg Phe Val Pro Val Val Ala Gly Ile Arg Ala
 115 120 125
 Ser Leu Arg Leu Gln Gly Arg Thr Met Ala Trp Arg His Leu Trp Val
 130 135 140
 Asp Gly Val Ser Leu Val Cys Pro Gly Leu Arg Ala Glu Gly Trp Thr
 145 150 155 160
 Pro Pro Pro Gly Ser Arg Val Leu Leu Lys Arg Cys Arg Ile Phe Ala
 165 170 175
 Ala Leu Glu Met His Val Cys Ser Phe Gly Arg Ser Pro Val Phe Ser
 180 185 190
 Cys Asn Cys Leu Pro Lys Ser Gln Ile Pro Pro Trp Ser Leu Val Cys
 195 200 205
 Gly Glu Gly Tyr Lys Ser Ser Pro Arg Met Pro Thr Leu Pro Pro Thr
 210 215 220
 Gly Ala Asp Ser Gly Tyr Pro
 225 230

<210> 155
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(264)

<400> 155

atg ctg atg ctg ttt ctt cag ttg tat ttt gtc act ctg gct ttc aga	48
Met Leu Met Leu Phe Leu Gln Leu Tyr Phe Val Thr Leu Ala Phe Arg	
1 5 10 15	
ggt ctc tat act ctc tca caa gcc ctg cct gac atc cac cag ctt cca	96
Val Leu Tyr Thr Leu Ser Gln Ala Leu Pro Asp Ile His Gln Leu Pro	
20 25 30	
gaa agg agc ccc ctt tgc ccc agc cgc cgt ttc tca aca gtt tct act	144
Glu Arg Ser Pro Leu Cys Pro Ser Arg Arg Phe Ser Thr Val Ser Thr	
35 40 45	
gct gcc att gct cag agg aca cag caa caa gga gcc atc ttg gaa gca	192
Ala Ala Ile Ala Gln Arg Thr Gln Gln Gln Gly Ala Ile Leu Glu Ala	
50 55 60	
gaa agc agc cct tac cag aca cca aac ttg tta gct cct cga tct tgg	240
Glu Ser Ser Pro Tyr Gln Thr Pro Asn Leu Leu Ala Pro Arg Ser Trp	
65 70 75 80	
att tcc tgg tgt cta gaa ctg tga	264
Ile Ser Trp Cys Leu Glu Leu *	
85	

<210> 156
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 156

Met Leu Met Leu Phe Leu Gln Leu Tyr Phe Val Thr Leu Ala Phe Arg
1 5 10 15

Val Leu Tyr Thr Leu Ser Gln Ala Leu Pro Asp Ile His Gln Leu Pro
 20 25 30
 Glu Arg Ser Pro Leu Cys Pro Ser Arg Arg Phe Ser Thr Val Ser Thr
 35 40 45
 Ala Ala Ile Ala Gln Arg Thr Gln Gln Gln Gly Ala Ile Leu Glu Ala
 50 55 60
 Glu Ser Ser Pro Tyr Gln Thr Pro Asn Leu Leu Ala Pro Arg Ser Trp
 65 70 75 80
 Ile Ser Trp Cys Leu Glu Leu
 85

<210> 157

<211> 258

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(258)

<400> 157

atg ctg act gcc atg ctt tcc ctc ctt ggc ttt ctc cag gca ctc ttc 48
 Met Leu Thr Ala Met Leu Ser Leu Leu Gly Phe Leu Gln Ala Leu Phe
 1 5 10 15

aca cac aga tgt gtc tac agt ggc agg ttt ggg agc ctg aag agc ggc 96
 Thr His Arg Cys Val Tyr Ser Gly Arg Phe Gly Ser Leu Lys Ser Gly
 20 25 30

tgt gcc cgg tac tgc aat gcc act gtg aag aac gtt ggc tcc aca agc 144
 Cys Ala Arg Tyr Cys Asn Ala Thr Val Lys Asn Val Gly Ser Thr Ser
 35 40 45

atg agc ctt cct ctg tct gtt cgc aca gtg tta gag cca gtc cag act 192
 Met Ser Leu Pro Leu Ser Val Arg Thr Val Leu Glu Pro Val Gln Thr
 50 55 60

cct tgg cta cct cca gac gta tgc agt agt tca tca tgc ctg caa gcg 240
 Pro Trp Leu Pro Pro Asp Val Cys Ser Ser Ser Ser Cys Leu Gln Ala
 65 70 75 80

gta acg aaa acg att tga 258
 Val Thr Lys Thr Ile *

85

<210> 158
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 158

Met Leu Thr Ala Met Leu Ser Leu Leu Gly Phe Leu Gln Ala Leu Phe
 1 5 10 15
 Thr His Arg Cys Val Tyr Ser Gly Arg Phe Gly Ser Leu Lys Ser Gly
 20 25 30
 Cys Ala Arg Tyr Cys Asn Ala Thr Val Lys Asn Val Gly Ser Thr Ser
 35 40 45
 Met Ser Leu Pro Leu Ser Val Arg Thr Val Leu Glu Pro Val Gln Thr
 50 55 60
 Pro Trp Leu Pro Pro Asp Val Cys Ser Ser Ser Ser Cys Leu Gln Ala
 65 70 75 80
 Val Thr Lys Thr Ile
 85

<210> 159
 <211> 624
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(624)

<400> 159

atg gtc cgc tgc ctg ggg cct gcg ctg ctg ctg ctg tta ctg ggg 48
 Met Val Arg Cys Leu Gly Pro Ala Leu Leu Leu Leu Leu Leu Gly
 1 5 10 15
 tcg gcg agc tcg gtc gga ggg aac cga tgt gtg gac gcg gcc gaa gcc 96
 Ser Ala Ser Ser Val Gly Gly Asn Arg Cys Val Asp Ala Ala Glu Ala
 20 25 30
 tgc acg gcg gac gcg cgg tgc cag cgt ttg cgc tcc gag tat gtg gcg 144
 Cys Thr Ala Asp Ala Arg Cys Gln Arg Leu Arg Ser Glu Tyr Val Ala
 35 40 45

cag tgc ctg ggc cgg gct gcg cag ggg ggc tgt ccc gcg ccc gct gcc 192
 Gln Cys Leu Gly Arg Ala Ala Gln Gly Gly Cys Pro Ala Pro Ala Ala
 50 55 60

gcc ggg ccc tgc gcc gct tct tcg ccc gcg ggc gcc cgc gct cac cca 240
 Ala Gly Pro Cys Ala Ala Ser Ser Pro Ala Gly Ala Arg Ala His Pro
 65 70 75 80

cgc act gct ctt ctg ccc gtg cgc cgc ccg gct gcg ccg agc gtc gga 288
 Arg Thr Ala Leu Leu Pro Val Arg Arg Pro Ala Ala Pro Ser Val Gly
 85 90 95

gca ccc ttc gtg ccc tcc tgc gcc ttt tcg ggg ccc ggc cgc ccg ccc 336
 Ala Pro Phe Val Pro Ser Cys Ala Phe Ser Gly Pro Gly Arg Pro Pro
 100 105 110

tcc tgc ctt gag ccc tta aac ttc tgc gag cga cgg aac tgc agg atc 384
 Ser Cys Leu Glu Pro Leu Asn Phe Cys Glu Arg Arg Asn Cys Arg Ile
 115 120 125

ccc ggc ggc gcg gcc gct ggc gag gcg ccc agc gcc ccc gac ggc tgc 432
 Pro Gly Gly Ala Ala Ala Gly Glu Ala Pro Ser Ala Pro Asp Gly Cys
 130 135 140

ctg ctg gac cag agg cgc ccg ctg cct gcg ccc tac gcg ggc ctc gtg 480
 Leu Leu Asp Gln Arg Arg Pro Leu Pro Ala Pro Tyr Ala Gly Leu Val
 145 150 155 160

ggt acg cgc ggc cgg gat ccg ggc gag ggc ggg ggt tct cca ggg gat 528
 Gly Thr Arg Gly Arg Asp Pro Gly Glu Gly Gly Gly Ser Pro Gly Asp
 165 170 175

atc tcc gcc ggc acc gcc gtc acc cct aac tac gtg gac aac gtg agc 576
 Ile Ser Ala Gly Thr Ala Val Thr Pro Asn Tyr Val Asp Asn Val Ser
 180 185 190

gcg cgt ggc gcc ctg gtg cga ctg cgg agc cag cgg gaa ccg gcg tga 624
 Ala Arg Gly Ala Leu Val Arg Leu Arg Ser Gln Arg Glu Pro Ala *
 195 200 205

160

<211> 207
 <212> PRT
 <213> Homo sapiens

<400> 160

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Met Val Arg Cys Leu Gly Pro Ala Leu Leu Leu Leu Leu Leu Gly
 1          5          10          15
Ser Ala Ser Ser Val Gly Gly Asn Arg Cys Val Asp Ala Ala Glu Ala
 20          25          30
Cys Thr Ala Asp Ala Arg Cys Gln Arg Leu Arg Ser Glu Tyr Val Ala
 35          40          45
Gln Cys Leu Gly Arg Ala Ala Gln Gly Gly Cys Pro Ala Pro Ala Ala
 50          55          60
Ala Gly Pro Cys Ala Ala Ser Ser Pro Ala Gly Ala Arg Ala His Pro
 65          70          75          80
Arg Thr Ala Leu Leu Pro Val Arg Arg Pro Ala Ala Pro Ser Val Gly
 85          90          95
Ala Pro Phe Val Pro Ser Cys Ala Phe Ser Gly Pro Gly Arg Pro Pro
100          105          110
Ser Cys Leu Glu Pro Leu Asn Phe Cys Glu Arg Arg Asn Cys Arg Ile
115          120          125
Pro Gly Gly Ala Ala Ala Gly Glu Ala Pro Ser Ala Pro Asp Gly Cys
130          135          140
Leu Leu Asp Gln Arg Arg Pro Leu Pro Ala Pro Tyr Ala Gly Leu Val
145          150          155          160
Gly Thr Arg Gly Arg Asp Pro Gly Glu Gly Gly Gly Ser Pro Gly Asp
165          170          175
Ile Ser Ala Gly Thr Ala Val Thr Pro Asn Tyr Val Asp Asn Val Ser
180          185          190
Ala Arg Gly Ala Leu Val Arg Leu Arg Ser Gln Arg Glu Pro Ala
195          200          205

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<210> 161
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(423)

<400> 161

atg tcc acc acc aca tgc caa gtg gtg gcg ttc ctc ctg tcc atc ctg

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile	Leu	
1				5					10					15		
ggg	ctg	gcc	ggc	tgc	atc	gcg	gcc	acc	ggg	atg	gac	atg	tgg	agc	acc	96
Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp	Ser	Thr	
			20					25					30			
cag	gac	ctg	tac	gac	aac	ccc	gtc	acc	tcc	gtg	ttc	cag	tac	gaa	ggg	144
Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln	Tyr	Glu	Gly	
			35				40					45				
ctc	tgg	agg	agc	tgc	gtg	agg	cag	agt	tca	ggc	ttc	acc	gaa	tgc	agg	192
Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe	Thr	Glu	Cys	Arg	
	50					55					60					
ccc	tat	ttc	acc	atc	ctg	gga	ctt	cca	gtc	tct	tac	tcc	ccc	atc	ctg	240
Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Val	Ser	Tyr	Ser	Pro	Ile	Leu	
	65				70					75				80		
ttt	ctt	ctg	tcc	ttt	cag	tat	acc	ttg	gac	ttg	gtc	ctg	gac	atc	cat	288
Phe	Leu	Leu	Ser	Phe	Gln	Tyr	Thr	Leu	Asp	Leu	Val	Leu	Asp	Ile	His	
				85					90					95		
tgc	tcc	tgc	tcc	cct	gaa	ttc	ccc	cct	cca	cca	ccc	caa	ctg	tcc	tct	336
Cys	Ser	Cys	Ser	Pro	Glu	Phe	Pro	Pro	Pro	Pro	Pro	Gln	Leu	Ser	Ser	
				100				105					110			
cac	aaa	tct	tcc	tcc	aaa	cct	cct	caa	gcc	ccc	aaa	ttg	aat	aaa	gat	384
His	Lys	Ser	Ser	Ser	Lys	Pro	Pro	Gln	Ala	Pro	Lys	Leu	Asn	Lys	Asp	
			115				120					125				
tcc	aca	agt	ctc	tgt	acc	aaa	ccc	aga	gca	ttc	tca	tag				423
Ser	Thr	Ser	Leu	Cys	Thr	Lys	Pro	Arg	Ala	Phe	Ser	*				
	130					135					140					

<210> 162

<211> 140

<212> PRT

<213> Homo sapiens

<400> 162

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu

1 5 10 15
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35 40 45
 Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50 55 60
 Pro Tyr Phe Thr Ile Leu Gly Leu Pro Val Ser Tyr Ser Pro Ile Leu
 65 70 75 80
 Phe Leu Leu Ser Phe Gln Tyr Thr Leu Asp Leu Val Leu Asp Ile His
 85 90 95
 Cys Ser Cys Ser Pro Glu Phe Pro Pro Pro Pro Gln Leu Ser Ser
 100 105 110
 His Lys Ser Ser Ser Lys Pro Pro Gln Ala Pro Lys Leu Asn Lys Asp
 115 120 125
 Ser Thr Ser Leu Cys Thr Lys Pro Arg Ala Phe Ser
 130 135 140

<210> 163

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(612)

<400> 163

atg gtc cgg ctc tgc cag gcc ctg ctg ctg tta gtg gcc act gtg gcc 48
 Met Val Arg Leu Cys Gln Ala Leu Leu Leu Leu Val Ala Thr Val Ala
 1 5 10 15

ctt gca tcc aga aga ttc caa gcc tgg ggc tca aca aag gtg gtg agg 96
 Leu Ala Ser Arg Arg Phe Gln Ala Trp Gly Ser Thr Lys Val Val Arg
 20 25 30

aca ttc caa gat atc cct caa aac tac gtc tat gtg cag cag gca ctc 144
 Thr Phe Gln Asp Ile Pro Gln Asn Tyr Val Tyr Val Gln Gln Ala Leu
 35 40 45

tgg ttc gcc atg aag gag tat aac aag gcc agc ttt agt ata aca agt 192
 Trp Phe Ala Met Lys Glu Tyr Asn Lys Ala Ser Phe Ser Ile Thr Ser
 50 55 60

tca gct tta gga ctg agt gct gct gca gag ttt gtg caa tgt gag tgc	240
Ser Ala Leu Gly Leu Ser Ala Ala Ala Glu Phe Val Gln Cys Glu Cys	
65 70 75 80	
tgg cgc aag gag cat ctc atc ccc agc ggc ctg gag cca cac ggc aat	288
Trp Arg Lys Glu His Leu Ile Pro Ser Gly Leu Glu Pro His Gly Asn	
85 90 95	
gag aga att cca gta tac ttg gca cca ggg ctg gtt gct ttc cac agg	336
Glu Arg Ile Pro Val Tyr Leu Ala Pro Gly Leu Val Ala Phe His Arg	
100 105 110	
tgc act cag gtg aca gat agt ttg gag tac tat att gag gtc aaa att	384
Cys Thr Gln Val Thr Asp Ser Leu Glu Tyr Tyr Ile Glu Val Lys Ile	
115 120 125	
gcc cga aca att tgc aag aaa att tca gaa gat gaa aac tgt gca ttt	432
Ala Arg Thr Ile Cys Lys Lys Ile Ser Glu Asp Glu Asn Cys Ala Phe	
130 135 140	
caa gag gat ccc aaa atg caa aag tct cag agg tcc agg ctg ctg ctg	480
Gln Glu Asp Pro Lys Met Gln Lys Ser Gln Arg Ser Arg Leu Leu Leu	
145 150 155 160	
ctt cag gcc aag atg ggg gac agc ccc agc cag gcc agg ctg ttt tca	528
Leu Gln Ala Lys Met Gly Asp Ser Pro Ser Gln Ala Arg Leu Phe Ser	
165 170 175	
gat gga gac tgt cac aaa ggc aag ttc atc aca gag gag aca ggc tta	576
Asp Gly Asp Cys His Lys Gly Lys Phe Ile Thr Glu Glu Thr Gly Leu	
180 185 190	
ata aaa aag tcc ctt act ctc ctc gta gtt gac taa	612
Ile Lys Lys Ser Leu Thr Leu Leu Val Val Asp *	
195 200	

<210> 164

<211> 203

<212> PRT

<213> Homo sapiens

Met	Val	Arg	Leu	Cys	Gln	Ala	Leu	Leu	Leu	Val	Ala	Thr	Val	Ala	
1				5				10					15		
Leu	Ala	Ser	Arg	Arg	Phe	Gln	Ala	Trp	Gly	Ser	Thr	Lys	Val	Val	Arg
			20					25					30		
Thr	Phe	Gln	Asp	Ile	Pro	Gln	Asn	Tyr	Val	Tyr	Val	Gln	Gln	Ala	Leu
		35					40					45			
Trp	Phe	Ala	Met	Lys	Glu	Tyr	Asn	Lys	Ala	Ser	Phe	Ser	Ile	Thr	Ser
	50					55				60					
Ser	Ala	Leu	Gly	Leu	Ser	Ala	Ala	Ala	Glu	Phe	Val	Gln	Cys	Glu	Cys
65					70					75					80
Trp	Arg	Lys	Glu	His	Leu	Ile	Pro	Ser	Gly	Leu	Glu	Pro	His	Gly	Asn
				85					90					95	
Glu	Arg	Ile	Pro	Val	Tyr	Leu	Ala	Pro	Gly	Leu	Val	Ala	Phe	His	Arg
			100					105					110		
Cys	Thr	Gln	Val	Thr	Asp	Ser	Leu	Glu	Tyr	Tyr	Ile	Glu	Val	Lys	Ile
		115					120					125			
Ala	Arg	Thr	Ile	Cys	Lys	Lys	Ile	Ser	Glu	Asp	Glu	Asn	Cys	Ala	Phe
	130					135					140				
Gln	Glu	Asp	Pro	Lys	Met	Gln	Lys	Ser	Gln	Arg	Ser	Arg	Leu	Leu	Leu
145					150					155					160
Leu	Gln	Ala	Lys	Met	Gly	Asp	Ser	Pro	Ser	Gln	Ala	Arg	Leu	Phe	Ser
				165					170					175	
Asp	Gly	Asp	Cys	His	Lys	Gly	Lys	Phe	Ile	Thr	Glu	Glu	Thr	Gly	Leu
			180					185					190		
Ile	Lys	Lys	Ser	Leu	Thr	Leu	Leu	Val	Val	Asp					
		195					200								

<213> Homo sapiens

<222> (1)...(534)

atg ggt att cag aac tca cca gca ctc ctc ctg atg gct gtc att gtg
Met Gly Ile Gln Asn Ser Pro Ala Leu Leu Leu Met Ala Val Ile Val
1 5 10 15

ttt ggc acc ttt gct qta agt qta gac agt gac ttg tac act gaa ctg

96

[illegible]

<210> 166
 <211> 177
 <212> PRT
 <213> Homo sapiens

<400> 166

Met Gly Ile Gln Asn Ser Pro Ala Leu Leu Leu Met Ala Val Ile Val
 1 5 10 15
 Phe Gly Thr Phe Ala Val Ser Val Asp Ser Asp Leu Tyr Thr Glu Leu
 20 25 30
 Arg Cys Val Tyr Val Lys Ser Thr Phe Val Leu His Pro Arg Asn Ile
 35 40 45
 His Asn Leu Glu Leu Val Ser Ala Gly Pro His Cys Ser Lys Asp Glu
 50 55 60
 Val Met Met Glu Gln Cys Leu Ser Leu Gly Ser Ser Lys Met Gln Asn
 65 70 75 80
 Leu Ser His Glu Pro Ala Met Gln Arg Glu Glu Gly Arg Tyr Ala Gly
 85 90 95
 Tyr Lys Arg Arg Gly His Val Ile Gln Pro Trp Leu Pro Arg Thr Leu
 100 105 110
 Thr Leu Asn Ser Asn Phe Asp Thr Asp Asn Leu Leu Pro Pro Asn Gly
 115 120 125
 Lys Arg Lys Gln Gly Ile Leu Ser Val Ile Arg Glu Tyr Ala Lys Gln
 130 135 140
 Gly Thr Ser Arg Thr Phe Phe Ser Gly Ile Arg Asp Asp Gly Cys Thr
 145 150 155 160
 Phe Thr Glu Ser Met Met Leu Asp Val His Glu Ile Thr Leu Asn Arg
 165 170 175
 Lys

<210> 167
 <211> 555
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(555)

<400> 167

atg ctg agc aaa act gaa caa gtg cag ctg gga atg gcg ttg gcc ctg

Met	Leu	Ser	Lys	Thr	Glu	Gln	Val	Gln	Leu	Gly	Met	Ala	Leu	Ala	Leu	
1				5					10					15		
<p>gct gcc ttg agc aga ggc aga tct gtc ctg gcc ttc ctc ctg atc tct 96</p> <p>Ala Ala Leu Ser Arg Gly Arg Ser Val Leu Ala Phe Leu Leu Ile Ser</p> <p>20 25 30</p>																
<p>ggc gaa gat gca gaa ggc aaa tgc tta gca ttt tat ctg ttc tgc atc 144</p> <p>Gly Glu Asp Ala Glu Gly Lys Cys Leu Ala Phe Tyr Leu Phe Cys Ile</p> <p>35 40 45</p>																
<p>cca ccg gcg ggc ata att ccc agc tta gtc ttt gac aag tct tcc aag 192</p> <p>Pro Pro Ala Gly Ile Ile Pro Ser Leu Val Phe Asp Lys Ser Ser Lys</p> <p>50 55 60</p>																
<p>cct cag gcc cca gag ccc atg acg cca gca cgc tcc ttt tgg acg gtt 240</p> <p>Pro Gln Ala Pro Glu Pro Met Thr Pro Ala Arg Ser Phe Trp Thr Val</p> <p>65 70 75 80</p>																
<p>gtt tat gtc gtc gtt atc tat cag aac agc acc tat tac gat gga ggt 288</p> <p>Val Tyr Val Val Val Ile Tyr Gln Asn Ser Thr Tyr Tyr Asp Gly Gly</p> <p>85 90 95</p>																
<p>ggc tgc cat aac agc ctt aag gtg acc agc agc ccc gcc att gcc atc 336</p> <p>Gly Cys His Asn Ser Leu Lys Val Thr Ser Ser Pro Ala Ile Ala Ile</p> <p>100 105 110</p>																
<p>gcc acc gcc gcc gcc gct gcc atg gtc tcc gtg gac cct gag aac ctc 384</p> <p>Ala Thr Ala Ala Ala Ala Ala Met Val Ser Val Asp Pro Glu Asn Leu</p> <p>115 120 125</p>																
<p>cgg ggc ccg tcc ccc tcc agc gtg cag ccg cgc cac ttc ctg acc ttg 432</p> <p>Arg Gly Pro Ser Pro Ser Ser Val Gln Pro Arg His Phe Leu Thr Leu</p> <p>130 135 140</p>																
<p>gca ccc atc aaa ata ccc ctc cgg acg tcc ccc gtc tca ggc atg cgt 480</p> <p>Ala Pro Ile Lys Ile Pro Leu Arg Thr Ser Pro Val Ser Gly Met Arg</p> <p>145 150 155 160</p>																
<p>gtc cat cca cta act gta acc tgc acg ctt cgt gac cca gac atc ctt 528</p> <p>Val His Pro Leu Thr Val Thr Cys Thr Leu Arg Asp Pro Asp Ile Leu</p> <p>165 170 175</p>																

gtg aaa tgc gtg ttt ctt caa act tag
 Val Lys Cys Val Phe Leu Gln Thr *
 180

555

<210> 168
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 168

Met Leu Ser Lys Thr Glu Gln Val Gln Leu Gly Met Ala Leu Ala Leu
 1 5 10 15
 Ala Ala Leu Ser Arg Gly Arg Ser Val Leu Ala Phe Leu Leu Ile Ser
 20 25 30
 Gly Glu Asp Ala Glu Gly Lys Cys Leu Ala Phe Tyr Leu Phe Cys Ile
 35 40 45
 Pro Pro Ala Gly Ile Ile Pro Ser Leu Val Phe Asp Lys Ser Ser Lys
 50 55 60
 Pro Gln Ala Pro Glu Pro Met Thr Pro Ala Arg Ser Phe Trp Thr Val
 65 70 75 80
 Val Tyr Val Val Val Ile Tyr Gln Asn Ser Thr Tyr Tyr Asp Gly Gly
 85 90 95
 Gly Cys His Asn Ser Leu Lys Val Thr Ser Ser Pro Ala Ile Ala Ile
 100 105 110
 Ala Thr Ala Ala Ala Ala Ala Met Val Ser Val Asp Pro Glu Asn Leu
 115 120 125
 Arg Gly Pro Ser Pro Ser Ser Val Gln Pro Arg His Phe Leu Thr Leu
 130 135 140
 Ala Pro Ile Lys Ile Pro Leu Arg Thr Ser Pro Val Ser Gly Met Arg
 145 150 155 160
 Val His Pro Leu Thr Val Thr Cys Thr Leu Arg Asp Pro Asp Ile Leu
 165 170 175
 Val Lys Cys Val Phe Leu Gln Thr
 180

<210> 169
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<400> 169

atg gct ctc cgg gtc agc ctg tgt ctt ctc ctc cgt gca tcc tca ctt	48
Met Ala Leu Arg Val Ser Leu Cys Leu Leu Leu Arg Ala Ser Ser Leu	
1 5 10 15	
agc tgt gct gca cca gga aac ccc atg gct gga aac cgt aag ctc ccc	96
Ser Cys Ala Ala Pro Gly Asn Pro Met Ala Gly Asn Arg Lys Leu Pro	
20 25 30	
aag gaa gaa ggg act act tct tac cac aag ggt gaa gat gag tca ttt	144
Lys Glu Glu Gly Thr Thr Ser Tyr His Lys Gly Glu Asp Glu Ser Phe	
35 40 45	
gtc aat act tca aca gaa aag aaa atg agt aaa gat tgg aag tct gat	192
Val Asn Thr Ser Thr Glu Lys Lys Met Ser Lys Asp Trp Lys Ser Asp	
50 55 60	
gac agc atg cct gtc tgt agc tct gga aag ggc atg ggc atc tca aca	240
Asp Ser Met Pro Val Cys Ser Ser Gly Lys Gly Met Gly Ile Ser Thr	
65 70 75 80	
ggc ata cag gag agc cac aaa gag cat ctc aga gac caa ggc aca cgg	288
Gly Ile Gln Glu Ser His Lys Glu His Leu Arg Asp Gln Gly Thr Arg	
85 90 95	
gac ttt gca tta ctt cca aag gtc atg gtc acc gtc aca att tcc atg	336
Asp Phe Ala Leu Leu Pro Lys Val Met Val Thr Val Thr Ile Ser Met	
100 105 110	
acc tta ctc atg ctg gca act ctg ctt gaa acg tcc tta act cat ctt	384
Thr Leu Leu Met Leu Ala Thr Leu Leu Glu Thr Ser Leu Thr His Leu	
115 120 125	
ctc cac ctg gaa aaa atc caa acc ttt gat gaa gtt tgg cac tat ggc	432
Leu His Leu Glu Lys Ile Gln Thr Phe Asp Glu Val Trp His Tyr Gly	
130 135 140	
cat gac agc ctc cag ata gga gaa ggg tct ggc ttc att gac att tcc	480
His Asp Ser Leu Gln Ile Gly Glu Gly Ser Gly Phe Ile Asp Ile Ser	
145 150 155 160	

170

acg gta gtg cat aca gcc ctc gag acc tac tca aga gag gac aaa aga 528
 Thr Val Val His Thr Ala Leu Glu Thr Tyr Ser Arg Glu Asp Lys Arg
 165 170 175

gag gct cgg gta gag ctt atc tag 552
 Glu Ala Arg Val Glu Leu Ile *
 180

<210> 170
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Ala Leu Arg Val Ser Leu Cys Leu Leu Leu Arg Ala Ser Ser Leu
 1 5 10 15
 Ser Cys Ala Ala Pro Gly Asn Pro Met Ala Gly Asn Arg Lys Leu Pro
 20 25 30
 Lys Glu Glu Gly Thr Thr Ser Tyr His Lys Gly Glu Asp Glu Ser Phe
 35 40 45
 Val Asn Thr Ser Thr Glu Lys Lys Met Ser Lys Asp Trp Lys Ser Asp
 50 55 60
 Asp Ser Met Pro Val Cys Ser Ser Gly Lys Gly Met Gly Ile Ser Thr
 65 70 75 80
 Gly Ile Gln Glu Ser His Lys Glu His Leu Arg Asp Gln Gly Thr Arg
 85 90 95
 Asp Phe Ala Leu Leu Pro Lys Val Met Val Thr Val Thr Ile Ser Met
 100 105 110
 Thr Leu Leu Met Leu Ala Thr Leu Leu Glu Thr Ser Leu Thr His Leu
 115 120 125
 Leu His Leu Glu Lys Ile Gln Thr Phe Asp Glu Val Trp His Tyr Gly
 130 135 140
 His Asp Ser Leu Gln Ile Gly Glu Gly Ser Gly Phe Ile Asp Ile Ser
 145 150 155 160
 Thr Val Val His Thr Ala Leu Glu Thr Tyr Ser Arg Glu Asp Lys Arg
 165 170 175
 Glu Ala Arg Val Glu Leu Ile
 180

<210> 171
 <211> 429
 <212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(429)

<400> 171

atg gag acc ttt cct ctg ctg ctg ctc agc ctg ggc ctg gtt ctt gca	48
Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val Leu Ala	
1 5 10 15	
 gaa gca tca gaa agc aca atg aag ata att aaa gaa gaa ttt aca gac	96
Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp	
20 25 30	
 gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa cag acc	144
Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr	
35 40 45	
 att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc agc ctc	192
Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu	
50 55 60	
 agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc aga agt	240
Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser	
65 70 75 80	
 tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac aaa gag	288
Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu	
85 90 95	
 tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca aac gga	336
Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly	
100 105 110	
 tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa gtg atg	384
Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met	
115 120 125	
 cgc agg gtc cac agg gcc ccc agc tgc aag ttg ggg gtt ctt taa	429
Arg Arg Val His Arg Ala Pro Ser Cys Lys Leu Gly Val Leu *	
130 135 140	

<400> 172

<210> 173

<211> 534

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(534)

<400> 173

48

96

agc tcg cag cgg aag tgt gag agg aga gtt tct gtg ccc ttc tcc ccc 144
 Ser Ser Gln Arg Lys Cys Glu Arg Arg Val Ser Val Pro Phe Ser Pro
 35 40 45

gcc aaa aag aaa acc caa agg gca aga aga aat ttg ggc caa aaa tgc 192
 Ala Lys Lys Lys Thr Gln Arg Ala Arg Arg Asn Leu Gly Gln Lys Cys
 50 55 60

cca aaa gct cgt cac ctt ttt aaa aaa tgg ggt ccc cgt cac aaa att 240
 Pro Lys Ala Arg His Leu Phe Lys Lys Trp Gly Pro Arg His Lys Ile
 65 70 75 80

gtg tcc acc ccc aac act tcc tgg ggg ggc caa agg tct ttg gaa aaa 288
 Val Ser Thr Pro Asn Thr Ser Trp Gly Gly Gln Arg Ser Leu Glu Lys
 85 90 95

agc ttt gcc aaa tca ctc tta gct ttg gac cca cgc tgg gcc gtc ttt 336
 Ser Phe Ala Lys Ser Leu Leu Ala Leu Asp Pro Arg Trp Ala Val Phe
 100 105 110

ggg gac ttt acg ggg gtc tcc agt ggg tta acc aag gaa gac aaa ggt 384
 Gly Asp Phe Thr Gly Val Ser Ser Gly Leu Thr Lys Glu Asp Lys Gly
 115 120 125

ttc gaa gat cca tct caa ggc cta ttg gtt ata aag agg ttt aag ggt 432
 Phe Glu Asp Pro Ser Gln Gly Leu Leu Val Ile Lys Arg Phe Lys Gly
 130 135 140

ttt aag ttg ggg cct ttc cga ttc cgg agg gaa ccc gtc atc ccg ata 480
 Phe Lys Leu Gly Pro Phe Arg Phe Arg Arg Glu Pro Val Ile Pro Ile
 145 150 155 160

aag cag ttg gga tac ccc agg ggc tct gct aga agc tca ggc cag ggt 528
 Lys Gln Leu Gly Tyr Pro Arg Gly Ser Ala Arg Ser Ser Gly Gln Gly
 165 170 175

ggt tga 534
 Gly *

<211> 177
 <212> PRT
 <213> Homo sapiens

<400> 174

Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Ser Phe Ala Gly Gly Ser Ser Arg Val Asp Leu Gln Ala Ala
 20 25 30
 Ser Ser Gln Arg Lys Cys Glu Arg Arg Val Ser Val Pro Phe Ser Pro
 35 40 45
 Ala Lys Lys Lys Thr Gln Arg Ala Arg Arg Asn Leu Gly Gln Lys Cys
 50 55 60
 Pro Lys Ala Arg His Leu Phe Lys Lys Trp Gly Pro Arg His Lys Ile
 65 70 75 80
 Val Ser Thr Pro Asn Thr Ser Trp Gly Gly Gln Arg Ser Leu Glu Lys
 85 90 95
 Ser Phe Ala Lys Ser Leu Leu Ala Leu Asp Pro Arg Trp Ala Val Phe
 100 105 110
 Gly Asp Phe Thr Gly Val Ser Ser Gly Leu Thr Lys Glu Asp Lys Gly
 115 120 125
 Phe Glu Asp Pro Ser Gln Gly Leu Leu Val Ile Lys Arg Phe Lys Gly
 130 135 140
 Phe Lys Leu Gly Pro Phe Arg Phe Arg Arg Glu Pro Val Ile Pro Ile
 145 150 155 160
 Lys Gln Leu Gly Tyr Pro Arg Gly Ser Ala Arg Ser Ser Gly Gln Gly
 165 170 175
 Gly

<210> 175
 <211> 468
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(468)

<400> 175

atg ggt ttg ggc tcg ctg ctt gct ttt tgg ccg gga agc cgg tgc gtc
 Met Gly Leu Gly Ser Leu Leu Ala Phe Trp Pro Gly Ser Arg Cys Val
 1 5 10 15

ccg ttg gtt gtg gtt tgg gcc tac cgc cgg gtg tgg cgg gtg ggt gct 96
 Pro Leu Val Val Val Trp Ala Tyr Arg Arg Val Trp Arg Val Gly Ala
 20 25 30

ggg gtc ccc ggg ggg ggt ggt cta ttt aaa aaa aaa aaa aag ctc ctc 144
 Gly Val Pro Gly Gly Gly Gly Leu Phe Lys Lys Lys Lys Lys Leu Leu
 35 40 45

gtt cgg aag gtt cga tcg gcc tta aag aac gcc tgc atg gtg ggt cta 192
 Val Arg Lys Val Arg Ser Ala Leu Lys Asn Ala Cys Met Val Gly Leu
 50 55 60

caa gtc att aaa tcc cag act gcc agc ggt cac aga agt cag gag aaa 240
 Gln Val Ile Lys Ser Gln Thr Ala Ser Gly His Arg Ser Gln Glu Lys
 65 70 75 80

gac ctg gaa cag att ctt tct cag agt atc aac aag gaa cca atc ctg 288
 Asp Leu Glu Gln Ile Leu Ser Gln Ser Ile Asn Lys Glu Pro Ile Leu
 85 90 95

cat gac tcc ttg ggg tac cga gct cga att cgt aat cat ggc atc ggc 336
 His Asp Ser Leu Gly Tyr Arg Ala Arg Ile Arg Asn His Gly Ile Gly
 100 105 110

gcc cgc gtt gtt ccg ggt ttg gct ggt gtt gtt cgg tct tct cgg tgc 384
 Ala Arg Val Val Pro Gly Leu Ala Gly Val Val Arg Ser Ser Arg Cys
 115 120 125

cgg cgt atg gcg gcc cta gtt tcg cgt cgc ggc acc ggc att ttt gtg 432
 Arg Arg Met Ala Ala Leu Val Ser Arg Arg Gly Thr Gly Ile Phe Val
 130 135 140

ttg tac gaa gcg gag gaa aag aag act gcg tgc tga 468
 Leu Tyr Glu Ala Glu Glu Lys Lys Thr Ala Cys *
 145 150 155

<210> 176

<211> 155

<212> PRT

<213> Homo sapiens

Met	Gly	Leu	Gly	Ser	Leu	Leu	Ala	Phe	Trp	Pro	Gly	Ser	Arg	Cys	Val
1				5					10					15	
Pro	Leu	Val	Val	Val	Trp	Ala	Tyr	Arg	Arg	Val	Trp	Arg	Val	Gly	Ala
			20					25					30		
Gly	Val	Pro	Gly	Gly	Gly	Gly	Leu	Phe	Lys	Lys	Lys	Lys	Lys	Leu	Leu
		35					40					45			
Val	Arg	Lys	Val	Arg	Ser	Ala	Leu	Lys	Asn	Ala	Cys	Met	Val	Gly	Leu
	50					55					60				
Gln	Val	Ile	Lys	Ser	Gln	Thr	Ala	Ser	Gly	His	Arg	Ser	Gln	Glu	Lys
65					70					75					80
Asp	Leu	Glu	Gln	Ile	Leu	Ser	Gln	Ser	Ile	Asn	Lys	Glu	Pro	Ile	Leu
				85					90					95	
His	Asp	Ser	Leu	Gly	Tyr	Arg	Ala	Arg	Ile	Arg	Asn	His	Gly	Ile	Gly
			100					105					110		
Ala	Arg	Val	Val	Pro	Gly	Leu	Ala	Gly	Val	Val	Arg	Ser	Ser	Arg	Cys
		115					120					125			
Arg	Arg	Met	Ala	Ala	Leu	Val	Ser	Arg	Arg	Gly	Thr	Gly	Ile	Phe	Val
	130					135					140				
Leu	Tyr	Glu	Ala	Glu	Glu	Lys	Lys	Thr	Ala	Cys					
145					150					155					

<211> 288

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(288)

<400> 177

atg	att	tta	tta	cac	ctt	ctg	gat	ttg	gca	aag	atc	aac	gct	caa	agt	48
Met	Ile	Leu	Leu	His	Leu	Leu	Asp	Leu	Ala	Lys	Ile	Asn	Ala	Gln	Ser	
1				5					10					15		
gcg	acg	gcc	tct	tcg	aat	tgg	gat	cgc	ccc	aag	cct	agg	aat	ctt	atc	96
Ala	Thr	Ala	Ser	Ser	Asn	Trp	Asp	Arg	Pro	Lys	Pro	Arg	Asn	Leu	Ile	
			20					25					30			
cct	ccg	att	tat	gcg	aac	ccg	aca	atg	tac	gtg	gag	cgg	gag	gtt	gct	144
Pro	Pro	Ile	Tyr	Ala	Asn	Pro	Thr	Met	Tyr	Val	Glu	Arg	Glu	Val	Ala	
		35					40					45				

atg gtg tgc ttc ctc aga gtg ctg tgg ctt ctc ctc ttg att ctc tct 48
 Met Val Cys Phe Leu Arg Val Leu Trp Leu Leu Leu Leu Ile Leu Ser
 1 5 10 15

 tct ctg cta acc cag aaa acc cgc act gct gag aag aaa tat ggc aca 96
 Ser Leu Leu Thr Gln Lys Thr Arg Thr Ala Glu Lys Lys Tyr Gly Thr
 20 25 30

 caa cag ttt ctt cct ctg ctc cat gct gga cca agt ggc ttc ata gct 144
 Gln Gln Phe Leu Pro Leu Leu His Ala Gly Pro Ser Gly Phe Ile Ala
 35 40 45

 gcc cag cca gag aca tca aca aca gcc atg ggt gcc aca gct agg agc 192
 Ala Gln Pro Glu Thr Ser Thr Thr Ala Met Gly Ala Thr Ala Arg Ser
 50 55 60

 ttc tac ctg gaa cat ccg tta gct ttt gag att cta ttt ttt gcc tta 240
 Phe Tyr Leu Glu His Pro Leu Ala Phe Glu Ile Leu Phe Phe Ala Leu
 65 70 75 80

 tat gtg agg gac tgc aat gtg gaa gaa agg agg agg gaa aca ccg gcc 288
 Tyr Val Arg Asp Cys Asn Val Glu Glu Arg Arg Arg Glu Thr Pro Ala
 85 90 95

 ctg ggc gcc agg tct cct cct cta gag ctc tcc cca gtt gtg acg ctc 336
 Leu Gly Ala Arg Ser Pro Pro Leu Glu Leu Ser Pro Val Val Thr Leu
 100 105 110

 tta ttc aag gcg ttc tcc ccc ccg gac aca gac ttg ctt cat cag cgt 384
 Leu Phe Lys Ala Phe Ser Pro Pro Asp Thr Asp Leu Leu His Gln Arg
 115 120 125

 aca gtg cag gct aaa cag tga 405
 Thr Val Gln Ala Lys Gln *
 130

<210> 180

<211> 134

<212> PRT

<213> Homo sapiens

<400> 180

Met Val Cys Phe Leu Arg Val Leu Trp Leu Leu Leu Ile Leu Ser
 1 5 10 15
 Ser Leu Leu Thr Gln Lys Thr Arg Thr Ala Glu Lys Lys Tyr Gly Thr
 20 25 30
 Gln Gln Phe Leu Pro Leu Leu His Ala Gly Pro Ser Gly Phe Ile Ala
 35 40 45
 Ala Gln Pro Glu Thr Ser Thr Thr Ala Met Gly Ala Thr Ala Arg Ser
 50 55 60
 Phe Tyr Leu Glu His Pro Leu Ala Phe Glu Ile Leu Phe Phe Ala Leu
 65 70 75 80
 Tyr Val Arg Asp Cys Asn Val Glu Glu Arg Arg Arg Glu Thr Pro Ala
 85 90 95
 Leu Gly Ala Arg Ser Pro Pro Leu Glu Leu Ser Pro Val Val Thr Leu
 100 105 110
 Leu Phe Lys Ala Phe Ser Pro Pro Asp Thr Asp Leu Leu His Gln Arg
 115 120 125
 Thr Val Gln Ala Lys Gln
 130

<210> 181

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(366)

<400> 181

atg gcg acg ccc agg ggc ctg ggg gcc ctg ctc ctg ctc ctc ctg ctc 48
 Met Ala Thr Pro Arg Gly Leu Gly Ala Leu Leu Leu Leu Leu Leu
 1 5 10 15

ccg acc tca ggg cca cag gca ccc agt ctg agc ttg tct ggg ctg gcg 96
 Pro Thr Ser Gly Pro Gln Ala Pro Ser Leu Ser Leu Ser Gly Leu Ala
 20 25 30

ggc agc ccc agc gaa tca cat gag gat gcc tgg ggc ggg ggg aca gag 144
 Gly Ser Pro Ser Glu Ser His Glu Asp Ala Trp Gly Gly Gly Thr Glu
 35 40 45

aac cac tct gaa aca cac tgt gcc aac caa aag gct ccc cgg act gtc 192
 Asn His Ser Glu Thr His Cys Ala Asn Gln Lys Ala Pro Arg Thr Val

50	55	60	
cca gca gtt ctg agg agt gcc tgt ccc cgt ttt aca gac aag gag atg			240
Pro Ala Val Leu Arg Ser Ala Cys Pro Arg Phe Thr Asp Lys Glu Met			
65	70	75	80
gag ggt gac cga aaa caa ctc aaa gca atc cac caa gcc tct agt cag			288
Glu Gly Asp Arg Lys Gln Leu Lys Ala Ile His Gln Ala Ser Ser Gln			
85	90	95	
cag ctg ctg tgt gtc aac tac cca gag gaa aca ggt gaa aac caa atg			336
Gln Leu Leu Cys Val Asn Tyr Pro Glu Glu Thr Gly Glu Asn Gln Met			
100	105	110	
tca aga ctg ggg gca gag gcc gtg gcc tag			366
Ser Arg Leu Gly Ala Glu Ala Val Ala *			
115	120		

<210> 182

<211> 121

<212> PRT

<213> Homo sapiens

<400> 182

Met Ala Thr Pro Arg Gly Leu Gly Ala Leu Leu Leu Leu Leu Leu			
1	5	10	15
Pro Thr Ser Gly Pro Gln Ala Pro Ser Leu Ser Leu Ser Gly Leu Ala			
20	25	30	
Gly Ser Pro Ser Glu Ser His Glu Asp Ala Trp Gly Gly Gly Thr Glu			
35	40	45	
Asn His Ser Glu Thr His Cys Ala Asn Gln Lys Ala Pro Arg Thr Val			
50	55	60	
Pro Ala Val Leu Arg Ser Ala Cys Pro Arg Phe Thr Asp Lys Glu Met			
65	70	75	80
Glu Gly Asp Arg Lys Gln Leu Lys Ala Ile His Gln Ala Ser Ser Gln			
85	90	95	
Gln Leu Leu Cys Val Asn Tyr Pro Glu Glu Thr Gly Glu Asn Gln Met			
100	105	110	
Ser Arg Leu Gly Ala Glu Ala Val Ala			
115	120		

<210> 183

<211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(693)

<400> 183

atg gat gat tgt gaa gta aat gac tta cat gaa ggg gca gga gtg aaa	48
Met Asp Asp Cys Glu Val Asn Asp Leu His Glu Gly Ala Gly Val Lys	
1 5 10 15	
cgg tcc ttc ctg atc acc ttg gtg tct cct ggt gca tta gga gcc agg	96
Arg Ser Phe Leu Ile Thr Leu Val Ser Pro Gly Ala Leu Gly Ala Arg	
20 25 30	
tgt gat gta aga gaa gga gag aga ggt ctt gtg aag act gag cga ggc	144
Cys Asp Val Arg Glu Gly Glu Arg Gly Leu Val Lys Thr Glu Arg Gly	
35 40 45	
ttg gtg aag caa ctc gac aag aga aac gac ctg tgc aaa ggg tgg acc	192
Leu Val Lys Gln Leu Asp Lys Arg Asn Asp Leu Cys Lys Gly Trp Thr	
50 55 60	
aca gcc cac aca ggt gtg tgc aaa cac acc gct cag cct gtc agg cat	240
Thr Ala His Thr Gly Val Cys Lys His Thr Ala Gln Pro Val Arg His	
65 70 75 80	
att tcc tca gag acc ctg gca cgg cca ggc cct cct cac ccc aac aat	288
Ile Ser Ser Glu Thr Leu Ala Arg Pro Gly Pro Pro His Pro Asn Asn	
85 90 95	
aca gag gag tgg ggt ctg gat gca ctt agg caa gac cta aac cac agc	336
Thr Glu Glu Trp Gly Leu Asp Ala Leu Arg Gln Asp Leu Asn His Ser	
100 105 110	
agt aag aca gca gct act ccc tgc tgc tac atc tgt gga caa gca ggt	384
Ser Lys Thr Ala Ala Thr Pro Cys Cys Tyr Ile Cys Gly Gln Ala Gly	
115 120 125	
cat gaa aat gtg tca gac agt ggt ggc agc tgg att cct gat tct gtg	432
His Glu Asn Val Ser Asp Ser Gly Gly Ser Trp Ile Pro Asp Ser Val	

<210> 184
<211> 230
<212> PRT
<213> Homo sapiens

<400> 184															
Met	Asp	Asp	Cys	Glu	Val	Asn	Asp	Leu	His	Glu	Gly	Ala	Gly	Val	Lys
1				5					10					15	
Arg	Ser	Phe	Leu	Ile	Thr	Leu	Val	Ser	Pro	Gly	Ala	Leu	Gly	Ala	Arg
			20					25					30		
Cys	Asp	Val	Arg	Glu	Gly	Glu	Arg	Gly	Leu	Val	Lys	Thr	Glu	Arg	Gly
		35					40					45			
Leu	Val	Lys	Gln	Leu	Asp	Lys	Arg	Asn	Asp	Leu	Cys	Lys	Gly	Trp	Thr
	50					55					60				
Thr	Ala	His	Thr	Gly	Val	Cys	Lys	His	Thr	Ala	Gln	Pro	Val	Arg	His
65					70					75					80

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<210> 185
<211> 1416
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1416)
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<400> 185																
atg	agg	ctt	ctc	ctg	gtg	ctg	ctg	ctt	ctg	gct	gct	gtg	tgt	gct	gcc	48
Met	Arg	Leu	Leu	Leu	Val	Leu	Leu	Leu	Leu	Ala	Ala	Val	Cys	Ala	Ala	
1				5					10					15		
ctg	gtt	ggc	cca	tat	gat	gct	gac	ggt	cag	aca	gca	cct	gct	ggg	agc	96
Leu	Val	Gly	Pro	Tyr	Asp	Ala	Asp	Gly	Gln	Thr	Ala	Pro	Ala	Gly	Ser	
			20					25					30			
tgg	tca	ctg	ctc	cca	gga	tct	aat	gag	ggt	gac	ccc	ttc	att	ccc	atc	144
Trp	Ser	Leu	Leu	Pro	Gly	Ser	Asn	Glu	Gly	Asp	Pro	Phe	Ile	Pro	Ile	
		35					40					45				

aca gcc cga ggg ctt agg gat tac cag gat ccc tac gga gaa gtg gcg	192
Thr Ala Arg Gly Leu Arg Asp Tyr Gln Asp Pro Tyr Gly Glu Val Ala	
50 55 60	
gta atg aca ccc cta cag aac acc tcc tac agg aca ccc cta cag aac	240
Val Met Thr Pro Leu Gln Asn Thr Ser Tyr Arg Thr Pro Leu Gln Asn	
65 70 75 80	
acc tcc tat agg acc ccc cta cag gat act ccc tac agg gcg tcc cta	288
Thr Ser Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Arg Ala Ser Leu	
85 90 95	
cag aac acc tcc tac agg ata ctc cct aca gga tac tcc cta cag gac	336
Gln Asn Thr Ser Tyr Arg Ile Leu Pro Thr Gly Tyr Ser Leu Gln Asp	
100 105 110	
act ctc tac agg aca cca cta cag gac act ccc tac aga aaa ccc cta	384
Thr Leu Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Arg Lys Pro Leu	
115 120 125	
cag gaa acc tcc tac agg aca ctc cct aca gga tac tcc cta cag aaa	432
Gln Glu Thr Ser Tyr Arg Thr Leu Pro Thr Gly Tyr Ser Leu Gln Lys	
130 135 140	
acc cct aca gga aac ttc cta cag gac act ccc tac agg ata ctc cct	480
Thr Pro Thr Gly Asn Phe Leu Gln Asp Thr Pro Tyr Arg Ile Leu Pro	
145 150 155 160	
aca gga tac tcc cta cag gaa acc ctc tac agg aca ctc cct aca gga	528
Thr Gly Tyr Ser Leu Gln Glu Thr Leu Tyr Arg Thr Leu Pro Thr Gly	
165 170 175	
cat tct cta cag gat act ccc tac aag aaa acc cta caa gat act cct	576
His Ser Leu Gln Asp Thr Pro Tyr Lys Lys Thr Leu Gln Asp Thr Pro	
180 185 190	
aca gaa aac ctc tac agg aca ctc cct aca gga cac tcc cta cag gaa	624
Thr Glu Asn Leu Tyr Arg Thr Leu Pro Thr Gly His Ser Leu Gln Glu	
195 200 205	
acc tcc tac agg aca ccc cct aca gga cac cac cta cag gaa acc cct	672
Thr Ser Tyr Arg Thr Pro Pro Thr Gly His His Leu Gln Glu Thr Pro	
210 215 220	

aca Thr 225	gga Gly	cac His	ccc Pro	tat Tyr	atg Met 230	aca Thr	ccc Pro	cta Leu	cag Gln	tac Tyr 235	acc Thr	ccc Pro	tat Tyr	agg Arg	aca Thr 240	720
cct Pro	gaa Glu	cag Gln	gac Asp	acc Thr 245	ccc Pro	tac Tyr	agg Arg	acg Thr	ctc Leu 250	cct Pro	aca Thr	gga Gly	cac His	tcc Ser 255	cta Leu	768
caa Gln	gac Asp	act Thr	ctt Leu 260	aca Thr	gga Gly	aac Asn	ctc Leu	tac Tyr 265	agg Arg	aca Thr	ctc Leu	cct Pro	aca Thr 270	ggc Gly	tcc Ser	816
cta Leu	cag Gln	gaa Glu 275	acc Thr	cct Pro	aca Thr	gga Gly	cct Pro 280	gcc Ala	tta Leu	cag Gln	gaa Glu	acc Thr 285	cct Pro	aca Thr	agg Arg	864
cgc Arg 290	tcc Ser	tac Tyr	agg Arg	aaa Lys	cct Pro	cca Pro 295	cag Gln	gac Asp	act Thr	ccc Pro 300	tac Tyr	aga Arg	aaa Lys	ccc Pro	cct Pro	912
aca Thr 305	gga Gly	cac His	tcc Ser	cta Leu 310	cag Gln	gac Asp	acc Thr	ccc Pro	tac Tyr 315	agg Arg	aca Thr	ctc Leu	cct Pro	aca Thr 320	gga Gly	960
cac His	ccc Pro	tac Tyr	agg Arg	aca Thr 325	ccc Pro	cta Leu	ctg Leu	gac Asp	acc Thr 330	cct Pro	ata Ile	gga Gly	cac His	tgt Cys 335	aca Thr	1008
gga Gly	cac His	ccc Pro	cta Leu 340	cag Gln	gac Asp	act Thr	ccc Pro	tac Tyr 345	agg Arg	aaa Lys	ccc Pro	cta Leu 350	caa Gln	gac Asp	act Thr	1056
cct Pro	aca Thr 355	gga Gly	aac Asn	ctc Leu	tac Tyr	agg Arg	aca Thr 360	ctc Leu	cct Pro	aca Thr	gga Gly	aac Asn 365	ccc Pro	cta Leu	cgg Arg	1104
gac Asp 370	act Thr	ccc Pro	tac Tyr	agg Arg	gca Ala	ccc Pro 375	cct Pro	aca Thr	gga Gly	cac His	ccc Pro 380	tac Tyr	agg Arg	acg Thr	atc Ile	1152
cct Pro	ata Ile	gga Gly	cac His	ctg Leu	tac Tyr	agg Arg	ata Ile	tcc Ser	cct Pro	aca Thr	gga Gly	cac His	tcc Ser	cta Leu	cag Gln	1200

385 390 395 400

gac act ctg cag gac gct cct aca aaa cac tcc ctg cag gac acc ccc 1248
 Asp Thr Leu Gln Asp Ala Pro Thr Lys His Ser Leu Gln Asp Thr Pro
 405 410 415

tac agg aca ccc tta cag gac act ccc tac aag aca ccc cct aca gga 1296
 Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Lys Thr Pro Pro Thr Gly
 420 425 430

cac cct tac agg aca ccc cta cag gac act ccc tac aag aca tcc cct 1344
 His Pro Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Lys Thr Ser Pro
 435 440 445

aca gga cac tcg tac agg aca cca cct aca gga cac ccc tac agg aca 1392
 Thr Gly His Ser Tyr Arg Thr Pro Pro Thr Gly His Pro Tyr Arg Thr
 450 455 460

cca cct aca gga tac ccc cta tag 1416
 Pro Pro Thr Gly Tyr Pro Leu *
 465 470

<210> 186
 <211> 471
 <212> PRT
 <213> Homo sapiens

<400> 186

Met Arg Leu Leu Leu Val Leu Leu Leu Leu Ala Ala Val Cys Ala Ala
 1 5 10 15

Leu Val Gly Pro Tyr Asp Ala Asp Gly Gln Thr Ala Pro Ala Gly Ser
 20 25 30

Trp Ser Leu Leu Pro Gly Ser Asn Glu Gly Asp Pro Phe Ile Pro Ile
 35 40 45

Thr Ala Arg Gly Leu Arg Asp Tyr Gln Asp Pro Tyr Gly Glu Val Ala
 50 55 60

Val Met Thr Pro Leu Gln Asn Thr Ser Tyr Arg Thr Pro Leu Gln Asn
 65 70 75 80

Thr Ser Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Arg Ala Ser Leu
 85 90 95

Gln Asn Thr Ser Tyr Arg Ile Leu Pro Thr Gly Tyr Ser Leu Gln Asp
 100 105 110

Thr	Leu	Tyr	Arg	Thr	Pro	Leu	Gln	Asp	Thr	Pro	Tyr	Arg	Lys	Pro	Leu	
		115					120					125				
Gln	Glu	Thr	Ser	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	Tyr	Ser	Leu	Gln	Lys	
		130					135				140					
Thr	Pro	Thr	Gly	Asn	Phe	Leu	Gln	Asp	Thr	Pro	Tyr	Arg	Ile	Leu	Pro	
145					150						155				160	
Thr	Gly	Tyr	Ser	Leu	Gln	Glu	Thr	Leu	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	
				165					170						175	
His	Ser	Leu	Gln	Asp	Thr	Pro	Tyr	Lys	Lys	Thr	Leu	Gln	Asp	Thr	Pro	
			180					185					190			
Thr	Glu	Asn	Leu	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	His	Ser	Leu	Gln	Glu	
		195					200					205				
Thr	Ser	Tyr	Arg	Thr	Pro	Pro	Thr	Gly	His	His	Leu	Gln	Glu	Thr	Pro	
		210				215					220					
Thr	Gly	His	Pro	Tyr	Met	Thr	Pro	Leu	Gln	Tyr	Thr	Pro	Tyr	Arg	Thr	
225					230					235					240	
Pro	Glu	Gln	Asp	Thr	Pro	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	His	Ser	Leu	
				245					250						255	
Gln	Asp	Thr	Leu	Thr	Gly	Asn	Leu	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	Ser	
			260					265					270			
Leu	Gln	Glu	Thr	Pro	Thr	Gly	Pro	Ala	Leu	Gln	Glu	Thr	Pro	Thr	Arg	
		275					280					285				
Arg	Ser	Tyr	Arg	Lys	Pro	Pro	Gln	Asp	Thr	Pro	Tyr	Arg	Lys	Pro	Pro	
		290				295					300					
Thr	Gly	His	Ser	Leu	Gln	Asp	Thr	Pro	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	
305					310					315					320	
His	Pro	Tyr	Arg	Thr	Pro	Leu	Leu	Asp	Thr	Pro	Ile	Gly	His	Cys	Thr	
				325					330						335	
Gly	His	Pro	Leu	Gln	Asp	Thr	Pro	Tyr	Arg	Lys	Pro	Leu	Gln	Asp	Thr	
			340					345					350			
Pro	Thr	Gly	Asn	Leu	Tyr	Arg	Thr	Leu	Pro	Thr	Gly	Asn	Pro	Leu	Arg	
		355					360					365				
Asp	Thr	Pro	Tyr	Arg	Ala	Pro	Pro	Thr	Gly	His	Pro	Tyr	Arg	Thr	Ile	
		370				375					380					
Pro	Ile	Gly	His	Leu	Tyr	Arg	Ile	Ser	Pro	Thr	Gly	His	Ser	Leu	Gln	
385					390					395					400	
Asp	Thr	Leu	Gln	Asp	Ala	Pro	Thr	Lys	His	Ser	Leu	Gln	Asp	Thr	Pro	
				405					410						415	
Tyr	Arg	Thr	Pro	Leu	Gln	Asp	Thr	Pro	Tyr	Lys	Thr	Pro	Pro	Thr	Gly	
			420					425					430			
His	Pro	Tyr	Arg	Thr	Pro	Leu	Gln	Asp	Thr	Pro	Tyr	Lys	Thr	Ser	Pro	
		435					440					445				
Thr	Gly	His	Ser	Tyr	Arg	Thr	Pro	Pro	Thr	Gly</						

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<210> 187
<211> 525
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(525)
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<400> 187																
atg	aag	acg	ctg	tgg	ctc	ctt	ctg	tct	ctt	gct	ctg	ttt	atc	ttt	cct	48
Met	Lys	Thr	Leu	Trp	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Phe	Ile	Phe	Pro	
1			5			10			15							
ttc	ttg	gcg	gtg	tgt	tct	gga	agt	ggc	tgc	atc	cct	gac	tct	gtg	gtg	96
Phe	Leu	Ala	Val	Cys	Ser	Gly	Ser	Gly	Cys	Ile	Pro	Asp	Ser	Val	Val	
20			25			30										
gag	tgt	ccg	gaa	ggg	gct	gtc	tgc	ccc	aca	gct	gca	gct	ccc	gag	gca	144
Glu	Cys	Pro	Glu	Gly	Ala	Val	Cys	Pro	Thr	Ala	Ala	Ala	Pro	Glu	Ala	
35			40			45										
ccc	gcc	cct	cca	cca	tgc	tca	cag	gtc	cct	ttc	atc	ccc	tcc	agc	cct	192
Pro	Ala	Pro	Pro	Pro	Cys	Ser	Gln	Val	Pro	Phe	Ile	Pro	Ser	Ser	Pro	
50			55			60										
agg	agt	gct	cta	tcc	aaa	gaa	gtc	tgg	cca	att	gga	tgc	agt	aca	tct	240
Arg	Ser	Ala	Leu	Ser	Lys	Glu	Val	Trp	Pro	Ile	Gly	Cys	Ser	Thr	Ser	
65			70			75			80							
ttt	ggg	atg	cag	aag	gtg	aat	ctc	ata	att	ggg	tct	att	ttt	cca	gtg	288
Phe	Gly	Met	Gln	Lys	Val	Asn	Leu	Ile	Ile	Gly	Ser	Ile	Phe	Pro	Val	
85			90			95										
tct	gca	ttc	ctc	ctg	aag	gat	gaa	gat	aac	tgc	tgt	gtc	cct	ttc	ctg	336
Ser	Ala	Phe	Leu	Leu	Lys	Asp	Glu	Asp	Asn	Cys	Cys	Val	Pro	Phe	Leu	
100			105			110										
ctc	aat	gaa	act	ctg	caa	atc	cta	cga	agc	cct	ttt	acc	aca	tgg	gga	384
Leu	Asn	Glu	Thr	Leu	Gln	Ile	Leu	Arg	Ser	Pro	Phe	Thr	Thr	Trp	Gly	

<210> 189
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(432)

<400> 189

atg gcc ccg ccg ctc ctg ctg ctg ctg ctg gcc agt gga gcg gcc gcc	48
Met Ala Pro Pro Leu Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala	
1 5 10 15	
tgc ccg ctg ccc tgc gtc tgc cag aac ctg tcc gag tcg ctc agc acc	96
Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr	
20 25 30	
ctc tgt gcc cac cga ggc ctg ctg ttt gtg ccg ccc aac gtg gac cgg	144
Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg	
35 40 45	
cgc aca gtg gag ctg cgg ctg gct gac aac ttc atc cag gcc ctg ggg	192
Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly	
50 55 60	
ccc cct gac ttc cgc aac atg acg gga ctg gtg gac ctg aca ctg tct	240
Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser	
65 70 75 80	
cgc aat gcc atc acc cgc att ggg gcc cgc gcc ttt ggg gac ctc gag	288
Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu	
85 90 95	
agc ctg cgt tcc ctc cac ctt gac ggc aac agg ctg gtg gag ctg ggc	336
Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly	
100 105 110	
acc ggg agc ctc cgg ggc ccc gtc aat ctg cag cac ctc atc ctc agc	384
Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser	
115 120 125	

ggc aac cag ctg ggc gca tcg cgc cgg gag cct tcg acg act tcc tag
 Gly Asn Gln Leu Gly Ala Ser Arg Arg Glu Pro Ser Thr Thr Ser *
 130 135 140

432

<210> 190
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Ala Pro Pro Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala
 1 5 10 15
 Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr
 20 25 30
 Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg
 35 40 45
 Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly
 50 55 60
 Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser
 65 70 75 80
 Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu
 85 90 95
 Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly
 100 105 110
 Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser
 115 120 125
 Gly Asn Gln Leu Gly Ala Ser Arg Arg Glu Pro Ser Thr Thr Ser
 130 135 140

<210> 191
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(357)

<400> 191
 atg ggt gta ggc aca gca tcc gtc cta aag aac tgt ctc ttc ctg ggc
 Met Gly Val Gly Thr Ala Ser Val Leu Lys Asn Cys Leu Phe Leu Gly
 1 5 10 15

48


```
<210> 193
<211> 324
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(324)
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<400> 193																	
atg	gtt	ctc	aaa	gtg	ccg	acg	tcc	aaa	gtc	ctg	cta	gtc	ctg	gcc	acc		48
Met	Val	Leu	Lys	Val	Pro	Thr	Ser	Lys	Val	Leu	Leu	Val	Leu	Ala	Thr		
1			5			10			15								
ttg	ttc	gcc	gtg	gcg	gcg	atg	atc	agc	agc	tgg	atg	ccc	cag	gtg	gcg		96
Leu	Phe	Ala	Val	Ala	Ala	Met	Ile	Ser	Ser	Trp	Met	Pro	Gln	Val	Ala		
20			25			30											
gcc	agt	ccg	ctc	gca	ccc	acg	gaa	tac	gaa	cag	aga	cgc	atg	atg	tgc		144
Ala	Ser	Pro	Leu	Ala	Pro	Thr	Glu	Tyr	Glu	Gln	Arg	Arg	Met	Met	Cys		
35			40			45											
tcc	acc	ggc	ctc	agc	gat	gtg	ata	cag	aag	ata	tgc	gta	agc	gga	acg		192
Ser	Thr	Gly	Leu	Ser	Asp	Val	Ile	Gln	Lys	Ile	Cys	Val	Ser	Gly	Thr		
50			55			60											
gtg	gcc	ctt	ggc	gat	gta	ttt	ccc	aac	agt	ttc	ggg	aag	cgc	agg	aag		240
Val	Ala	Leu	Gly	Asp	Val	Phe	Pro	Asn	Ser	Phe	Gly	Lys	Arg	Arg	Lys		
65			70			75			80								
cgc	gac	ttg	cag	aac	gta	acc	gat	ttg	tgc	tgc	aag	tcg	ggt	ggc	tgc		288
Arg	Asp	Leu	Gln	Asn	Val	Thr	Asp	Leu	Cys	Cys	Lys	Ser	Gly	Gly	Cys		
85			90			95											

acc tac agg gag ctc ttg cag tac tgc aaa gga tag
 Thr Tyr Arg Glu Leu Leu Gln Tyr Cys Lys Gly *
 100 105

324

<210> 194
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Val Leu Lys Val Pro Thr Ser Lys Val Leu Leu Val Leu Ala Thr
 1 5 10 15
 Leu Phe Ala Val Ala Ala Met Ile Ser Ser Trp Met Pro Gln Val Ala
 20 25 30
 Ala Ser Pro Leu Ala Pro Thr Glu Tyr Glu Gln Arg Arg Met Met Cys
 35 40 45
 Ser Thr Gly Leu Ser Asp Val Ile Gln Lys Ile Cys Val Ser Gly Thr
 50 55 60
 Val Ala Leu Gly Asp Val Phe Pro Asn Ser Phe Gly Lys Arg Arg Lys
 65 70 75 80
 Arg Asp Leu Gln Asn Val Thr Asp Leu Cys Cys Lys Ser Gly Gly Cys
 85 90 95
 Thr Tyr Arg Glu Leu Leu Gln Tyr Cys Lys Gly
 100 105

<210> 195
 <211> 498
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(498)

<400> 195
 atg cgg gaa gca ggt ggc ctt aaa gac aca act gga aag ctg tgg aaa
 Met Arg Glu Ala Gly Gly Leu Lys Asp Thr Thr Gly Lys Leu Trp Lys
 1 5 10 15

48

tca ttt ctg ctc cca agg gcg ctg ctg ccc tct ggt gcg cga gcc gcc
 Ser Phe Leu Leu Pro Arg Ala Leu Leu Pro Ser Gly Ala Arg Ala Ala

96

```
<210> 196
<211> 165
<212> PRT
<213> Homo sapiens
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<400> 196

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Met Arg Glu Ala Gly Gly Leu Lys Asp Thr Thr Gly Lys Leu Trp Lys
 1          5          10          15
Ser Phe Leu Leu Pro Arg Ala Leu Leu Pro Ser Gly Ala Arg Ala Ala
      20          25          30
Ser Gln Arg Leu His Leu Leu Leu Glu Thr Leu Thr Phe Pro Ala Val
      35          40          45
Ala Leu Ile Leu Gln Arg Val Lys Gly Gln Met Ser His Val Met Ser
      50          55          60
Ser Leu Pro Trp Asp Ser Arg Leu Tyr Leu Ala Leu Ile Ser Gly Ser
65          70          75          80
Ser Ala Trp Ile Ser Tyr Tyr Met Ile Met Leu Trp Ser Ile Ser Leu
      85          90          95
Ser Phe Phe Trp Val Pro Gly Phe Cys Asp Arg Leu Val Ala Phe Lys
      100          105          110
Lys Arg Leu Tyr Glu Ser Gln Phe Cys Gln Tyr Thr Ser Gly Tyr Lys
      115          120          125
Glu Asn Gln Asn Ile Ser Phe Val Asn Lys Asn Tyr Leu Leu Tyr Asn
      130          135          140
Tyr Ile Gly Ala Phe Cys Ile Leu Ala Val Leu Thr Tyr Gly Ser Arg
145          150          155          160
His Thr Leu Gly Val
      165

```

<210> 197

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(573)

<400> 197

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atg ctg ggc ctc ctg ggg agc aca gcc ctc gtg gga tgg atc aca ggt
Met Leu Gly Leu Leu Gly Ser Thr Ala Leu Val Gly Trp Ile Thr Gly
 1          5          10          15

```

48

```

gct gct gtg gcg gtc ctg ctg ctg ctg ctg ctg gcc acc tgc ctt
Ala Ala Val Ala Val Leu Leu Leu Leu Leu Leu Ala Thr Cys Leu
      20          25          30

```

96

ttc cac gga cgg cag gac tgt gac gtg gag agg aac cgt aca gct gca	144
Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg Thr Ala Ala	
35 40 45	
ggg gga aac cga gtc cgc cgg gcc cag cct tgg ccc ttc cgg cgg cgg	192
Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro Phe Arg Arg Arg	
50 55 60	
ggc cac ctg gga atc ttt cac cat cac cgt cat cct ggc cac gag acg	240
Gly His Leu Gly Ile Phe His His His Arg His Pro Gly His Glu Thr	
65 70 75 80	
gaa gga gag ccg ccg gag gag cac ggg gca cct gcg atc gcg aag agc	288
Glu Gly Glu Pro Pro Glu Glu His Gly Ala Pro Ala Ile Ala Lys Ser	
85 90 95	
ctc ctg ttc tgg atg gga gcg aag gct ccg aga gga cct aag gtt gct	336
Leu Leu Phe Trp Met Gly Ala Lys Ala Pro Arg Gly Pro Lys Val Ala	
100 105 110	
cag tgg gcc atg gaa acg gca gtg att ggg gtg gtg gtg ctg ttc	384
Gln Trp Ala Met Glu Thr Ala Val Ile Gly Val Val Val Val Leu Phe	
115 120 125	
gtg gtg act gtg gcc atc acc tgc gtc ctc tgc tgc ttc agc tgt gac	432
Val Val Thr Val Ala Ile Thr Cys Val Leu Cys Cys Phe Ser Cys Asp	
130 135 140	
tca agg gcc cag gat cct cag ggg ggt cct ggc cgc agc ttc acg gtg	480
Ser Arg Ala Gln Asp Pro Gln Gly Gly Pro Gly Arg Ser Phe Thr Val	
145 150 155 160	
gcc acg ttt cgc cag gaa gct tct ctc ttc acg ggg cct gtt cgc cat	528
Ala Thr Phe Arg Gln Glu Ala Ser Leu Phe Thr Gly Pro Val Arg His	
165 170 175	
gcc cag cca gtg cca agt gcc cag gac ttc tgg acc ttc atg tga	573
Ala Gln Pro Val Pro Ser Ala Gln Asp Phe Trp Thr Phe Met *	
180 185 190	

<210> 198

<211> 190

<212> PRT

<213> Homo sapiens

<400> 198

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Met Leu Gly Leu Leu Gly Ser Thr Ala Leu Val Gly Trp Ile Thr Gly
 1           5           10           15
Ala Ala Val Ala Val Leu Leu Leu Leu Leu Leu Ala Thr Cys Leu
 20           25           30
Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg Thr Ala Ala
 35           40           45
Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro Phe Arg Arg Arg
 50           55           60
Gly His Leu Gly Ile Phe His His His Arg His Pro Gly His Glu Thr
 65           70           75           80
Glu Gly Glu Pro Pro Glu Glu His Gly Ala Pro Ala Ile Ala Lys Ser
 85           90           95
Leu Leu Phe Trp Met Gly Ala Lys Ala Pro Arg Gly Pro Lys Val Ala
100           105           110
Gln Trp Ala Met Glu Thr Ala Val Ile Gly Val Val Val Val Leu Phe
115           120           125
Val Val Thr Val Ala Ile Thr Cys Val Leu Cys Cys Phe Ser Cys Asp
130           135           140
Ser Arg Ala Gln Asp Pro Gln Gly Gly Pro Gly Arg Ser Phe Thr Val
145           150           155           160
Ala Thr Phe Arg Gln Glu Ala Ser Leu Phe Thr Gly Pro Val Arg His
165           170           175
Ala Gln Pro Val Pro Ser Ala Gln Asp Phe Trp Thr Phe Met
180           185           190

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<210> 199

<211> 489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(489)

<400> 199

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atg gcg ctg cct cca ggc cca gcc gcc ctc cgg cac aca ctg ctg ctc
Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
 1           5           10           15

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$\langle 210 \rangle$	200
$\langle 211 \rangle$	162

<212> PRT

<213> Homo sapiens

<400> 200

Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
 1 5 10 15
 Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro Gln Ile
 20 25 30
 Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn Glu Arg His
 35 40 45
 Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr Pro Arg Leu Ala
 50 55 60
 Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser Arg Leu Leu
 65 70 75 80
 Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr Phe Thr Val
 85 90 95
 Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu Gln Asp Pro
 100 105 110
 Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn Val Gln Cys
 115 120 125
 Arg Glu Tyr Leu Leu Val Val Leu Phe Ala Leu Asp Arg Ala Asn Pro
 130 135 140
 Pro Ala Asn Val Thr Arg Asp Arg Pro Cys Leu Pro Ser Asp Cys Val
 145 150 155 160
 His Leu

<210> 201

<211> 1113

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1113)

<400> 201

atg aga act aaa acc cag caa cta aga ttt agg caa aga aaa cag att
 Met Arg Thr Lys Thr Gln Gln Leu Arg Phe Arg Gln Arg Lys Gln Ile
 1 5 10 15

48

cca gaa tca gca cag agc ctg ctg ctg ctg ctg ctt ctg tct gct
 Pro Glu Ser Ala Gln Ser Leu Leu Leu Leu Leu Leu Leu Ser Ala

96

20																25					30					
gct	tct	gct	gct	gga	ggc	att	gct	aac	aca	ctc	acc	caa	gcc	tta	gct	144										
Ala	Ser	Ala	Ala	Gly	Gly	Ile	Ala	Asn	Thr	Leu	Thr	Gln	Ala	Leu	Ala											
35				40				45																		
ctt	aat	aga	gac	atg	ttt	gca	gct	gaa	tgc	ccc	agt	gct	tgt	ggt	tta	192										
Leu	Asn	Arg	Asp	Met	Phe	Ala	Ala	Glu	Cys	Pro	Ser	Ala	Cys	Gly	Leu											
50				55				60																		
agc	aaa	att	gtt	aac	act	gtg	cga	agt	tca	tgg	cct	tct	gcc	aat	gcc	240										
Ser	Lys	Ile	Val	Asn	Thr	Val	Arg	Ser	Ser	Trp	Pro	Ser	Ala	Asn	Ala											
65				70				75				80														
att	gta	cag	tcc	ctg	aga	gaa	aaa	agg	aga	aag	ctc	ctt	ggg	ata	ata	288										
Ile	Val	Gln	Ser	Leu	Arg	Glu	Lys	Arg	Arg	Lys	Leu	Leu	Gly	Ile	Ile											
85				90				95																		
agg	cag	gtg	att	ctc	aga	ccc	ctc	agt	gga	gtt	tgt	ggg	tgg	cgg	cag	336										
Arg	Gln	Val	Ile	Leu	Arg	Pro	Leu	Ser	Gly	Val	Cys	Gly	Trp	Arg	Gln											
100				105				110																		
cag	tgg	tgg	tta	gtg	agg	aaa	gcc	cgt	ctt	cag	ggt	atg	tgc	aaa	tgc	384										
Gln	Trp	Trp	Leu	Val	Arg	Lys	Ala	Arg	Leu	Gln	Gly	Met	Cys	Lys	Cys											
115				120				125																		
acc	aca	gct	ttg	ctg	ctg	ggg	gag	ggt	ggg	gtt	gct	att	agt	ggc	agc	432										
Thr	Thr	Ala	Leu	Leu	Leu	Gly	Glu	Gly	Gly	Val	Ala	Ile	Ser	Gly	Ser											
130				135				140																		
agc	tgc	cgt	cag	ttg	gct	ctt	agg	ctc	tgg	gga	gca	tgt	gct	ttg	ggc	480										
Ser	Cys	Arg	Gln	Leu	Ala	Leu	Arg	Leu	Trp	Gly	Ala	Cys	Ala	Leu	Gly											
145				150				155				160														
ctt	ggt	ggt	ggc	tat	cat	ggt	gtc	agt	ggt	agc	agt	ggg	gag	tgg	cag	528										
Leu	Gly	Gly	Gly	Tyr	His	Gly	Val	Ser	Gly	Ser	Ser	Gly	Glu	Trp	Gln											
165				170				175																		
cag	cag	gga	gag	cca	gtt	ctc	agg	cgc	gcg	ctc	aaa	tgc	ctg	tgc	ttg	576										
Gln	Gln	Gly	Glu	Pro	Val	Leu	Arg	Arg	Ala	Leu	Lys	Cys	Leu	Cys	Leu											
180				185				190																		
cgt	tta	gga	agc	gac	gag	aat	ggg	tgg	ggt	caa	cac	aat	act	act	gct	624										

Arg	Leu	Gly	Ser	Asp	Glu	Asn	Gly	Trp	Gly	Gln	His	Asn	Thr	Thr	Ala	
	195						200					205				
gcc	cgc	tca	agg	ttg	aca	gag	tta	aat	gat	ttg	cag	gga	cca	ggc	act	672
Ala	Arg	Ser	Arg	Leu	Thr	Glu	Leu	Asn	Asp	Leu	Gln	Gly	Pro	Gly	Thr	
	210					215				220						
gtg	ggg	ggg	gta	tgg	ctg	ttt	tct	ctg	gcc	tcg	aaa	acc	att	ttc	tcc	720
Val	Gly	Gly	Val	Trp	Leu	Phe	Ser	Leu	Ala	Ser	Lys	Thr	Ile	Phe	Ser	
	225				230				235						240	
aga	gcc	gaa	cta	cgc	tct	aag	cac	cgg	aac	tac	ctt	att	agg	gat	aaa	768
Arg	Ala	Glu	Leu	Arg	Ser	Lys	His	Arg	Asn	Tyr	Leu	Ile	Arg	Asp	Lys	
			245					250					255			
tct	cgg	tct	agg	atc	tcg	cca	gaa	tct	cgt	gaa	cta	gtg	cta	agg	cac	816
Ser	Arg	Ser	Arg	Ile	Ser	Pro	Glu	Ser	Arg	Glu	Leu	Val	Leu	Arg	His	
			260					265					270			
aga	acc	cat	ttt	ggc	aca	gaa	aca	tac	tac	ttg	agg	tcg	aga	att	cta	864
Arg	Thr	His	Phe	Gly	Thr	Glu	Thr	Tyr	Tyr	Leu	Arg	Ser	Arg	Ile	Leu	
		275				280						285				
agg	ggg	aag	ctg	acc	ctc	cat	gtg	ata	ccc	gtt	gcg	gct	gtc	aga	cag	912
Arg	Gly	Lys	Leu	Thr	Leu	His	Val	Ile	Pro	Val	Ala	Ala	Val	Arg	Gln	
	290					295				300						
tat	ctt	acc	aca	agc	gac	ctt	cta	aat	agc	gtt	ttt	cta	tat	gat	gct	960
Tyr	Leu	Thr	Thr	Ser	Asp	Leu	Leu	Asn	Ser	Val	Phe	Leu	Tyr	Asp	Ala	
	305				310				315					320		
ggc	ggc	agc	cca	gtg	agg	gaa	gtg	caa	caa	gta	tgg	ttc	tcc	tgc	ttg	1008
Gly	Gly	Ser	Pro	Val	Arg	Glu	Val	Gln	Gln	Val	Trp	Phe	Ser	Cys	Leu	
			325					330						335		
tca	act	gtg	gaa	aca	gcg	acc	ctg	aaa	gtg	gag	gag	cca	cag	ctg	gaa	1056
Ser	Thr	Val	Glu	Thr	Ala	Thr	Leu	Lys	Val	Glu	Glu	Pro	Gln	Leu	Glu	
			340					345					350			
tcg	tgt	ccg	tct	gaa	tac	acg	cac	ctt	tcc	tat	gag	cct	tgt	aaa	gcc	1104
Ser	Cys	Pro	Ser	Glu	Tyr	Thr	His	Leu	Ser	Tyr	Glu	Pro	Cys	Lys	Ala	
		355					360					365				

agt cgt tga
 Ser Arg *
 370

<210> 202
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 202

Met Arg Thr Lys Thr Gln Gln Leu Arg Phe Arg Gln Arg Lys Gln Ile
 1 5 10 15
 Pro Glu Ser Ala Gln Ser Leu Leu Leu Leu Leu Leu Ser Ala
 20 25 30
 Ala Ser Ala Ala Gly Gly Ile Ala Asn Thr Leu Thr Gln Ala Leu Ala
 35 40 45
 Leu Asn Arg Asp Met Phe Ala Ala Glu Cys Pro Ser Ala Cys Gly Leu
 50 55 60
 Ser Lys Ile Val Asn Thr Val Arg Ser Ser Trp Pro Ser Ala Asn Ala
 65 70 75 80
 Ile Val Gln Ser Leu Arg Glu Lys Arg Arg Lys Leu Leu Gly Ile Ile
 85 90 95
 Arg Gln Val Ile Leu Arg Pro Leu Ser Gly Val Cys Gly Trp Arg Gln
 100 105 110
 Gln Trp Trp Leu Val Arg Lys Ala Arg Leu Gln Gly Met Cys Lys Cys
 115 120 125
 Thr Thr Ala Leu Leu Leu Gly Glu Gly Gly Val Ala Ile Ser Gly Ser
 130 135 140
 Ser Cys Arg Gln Leu Ala Leu Arg Leu Trp Gly Ala Cys Ala Leu Gly
 145 150 155 160
 Leu Gly Gly Gly Tyr His Gly Val Ser Gly Ser Ser Gly Glu Trp Gln
 165 170 175
 Gln Gln Gly Glu Pro Val Leu Arg Arg Ala Leu Lys Cys Leu Cys Leu
 180 185 190
 Arg Leu Gly Ser Asp Glu Asn Gly Trp Gly Gln His Asn Thr Thr Ala
 195 200 205
 Ala Arg Ser Arg Leu Thr Glu Leu Asn Asp Leu Gln Gly Pro Gly Thr
 210 215 220
 Val Gly Gly Val Trp Leu Phe Ser Leu Ala Ser Lys Thr Ile Phe Ser
 225 230 235 240
 Arg Ala Glu Leu Arg Ser Lys His Arg Asn Tyr Leu Ile Arg Asp Lys
 245 250 255

Ser Arg Ser Arg Ile Ser Pro Glu Ser Arg Glu Leu Val Leu Arg His
 260 265 270
 Arg Thr His Phe Gly Thr Glu Thr Tyr Tyr Leu Arg Ser Arg Ile Leu
 275 280 285
 Arg Gly Lys Leu Thr Leu His Val Ile Pro Val Ala Ala Val Arg Gln
 290 295 300
 Tyr Leu Thr Thr Ser Asp Leu Leu Asn Ser Val Phe Leu Tyr Asp Ala
 305 310 315 320
 Gly Gly Ser Pro Val Arg Glu Val Gln Gln Val Trp Phe Ser Cys Leu
 325 330 335
 Ser Thr Val Glu Thr Ala Thr Leu Lys Val Glu Glu Pro Gln Leu Glu
 340 345 350
 Ser Cys Pro Ser Glu Tyr Thr His Leu Ser Tyr Glu Pro Cys Lys Ala
 355 360 365
 Ser Arg
 370

<210> 203
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(279)

<400> 203
 atg gag ttg tgg tgg gag tgg gca ttg ctg gcc act ctc ctg gtg ctt 48
 Met Glu Leu Trp Trp Glu Trp Ala Leu Leu Ala Thr Leu Leu Val Leu
 1 5 10 15

 gtt gca ggg agc cag aaa ata tgt cag agt ata gag gac ccc cca tac 96
 Val Ala Gly Ser Gln Lys Ile Cys Gln Ser Ile Glu Asp Pro Pro Tyr
 20 25 30

 aat tta aag aat aag gag gag gag gag gag aag gag gag gag gga gag 144
 Asn Leu Lys Asn Lys Glu Glu Glu Glu Glu Lys Glu Glu Glu Gly Glu
 35 40 45

 gag aag gta gaa cat aac gtt tcc atc cag gtt aag aaa cag cca ggc 192
 Glu Lys Val Glu His Asn Val Ser Ile Gln Val Lys Lys Gln Pro Gly
 50 55 60

ctt ggt ctt ctg ctc ctg gac atc ccg gcc ttc act gac cac cgt ctg 240
 Leu Gly Leu Leu Leu Leu Asp Ile Pro Ala Phe Thr Asp His Arg Leu
 65 70 75 80

aac agg tcc gag ccc tgc tct acc ctg tgc ttt gct tga 279
 Asn Arg Ser Glu Pro Cys Ser Thr Leu Cys Phe Ala *
 85 90

<210> 204

<211> 92

<212> PRT

<213> Homo sapiens

<400> 204

Met Glu Leu Trp Trp Glu Trp Ala Leu Leu Ala Thr Leu Leu Val Leu
 1 5 10 15
 Val Ala Gly Ser Gln Lys Ile Cys Gln Ser Ile Glu Asp Pro Pro Tyr
 20 25 30
 Asn Leu Lys Asn Lys Glu Glu Glu Glu Lys Glu Glu Glu Gly Glu
 35 40 45
 Glu Lys Val Glu His Asn Val Ser Ile Gln Val Lys Lys Gln Pro Gly
 50 55 60
 Leu Gly Leu Leu Leu Leu Asp Ile Pro Ala Phe Thr Asp His Arg Leu
 65 70 75 80
 Asn Arg Ser Glu Pro Cys Ser Thr Leu Cys Phe Ala
 85 90

<210> 205

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(657)

<400> 205

atg cga gac aaa gca gcc cct gcc tgg aca gtg ctg gcc ctg atg caa 48
 Met Arg Asp Lys Ala Ala Pro Ala Trp Thr Val Leu Ala Leu Met Gln
 1 5 10 15

ggg gtg cag gca aag aag gag agg ccc tct tgg ctt cgg gat gca gtt 96

Gly	Val	Gln	Ala	Lys	Lys	Glu	Arg	Pro	Ser	Trp	Leu	Arg	Asp	Ala	Val		
			20					25						30			
ctc	tgc	tcc	acc	aca	cca	gtg	ccc	agg	gcc	ttt	ccc	atg	gca	aag	cac	144	
Leu	Cys	Ser	Thr	Thr	Pro	Val	Pro	Arg	Ala	Phe	Pro	Met	Ala	Lys	His		
		35					40				45						
caa	cac	ctg	ccc	tta	ttt	aaa	agc	tta	tct	gta	gcc	cag	cag	aaa	aca	192	
Gln	His	Leu	Pro	Leu	Phe	Lys	Ser	Leu	Ser	Val	Ala	Gln	Gln	Lys	Thr		
		50				55					60						
agg	cac	gac	aca	tat	ttg	agg	ttt	aac	atc	ttg	att	ctc	agg	ctt	tat	240	
Arg	His	Asp	Thr	Tyr	Leu	Arg	Phe	Asn	Ile	Leu	Ile	Leu	Arg	Leu	Tyr		
	65				70					75					80		
aac	act	gga	tat	tat	tgg	caa	cac	cat	gaa	aca	aag	aaa	cag	aag	ctt	288	
Asn	Thr	Gly	Tyr	Tyr	Trp	Gln	His	His	Glu	Thr	Lys	Lys	Gln	Lys	Leu		
				85				90					95				
ctg	ccc	act	cct	cca	cat	gtg	aca	tta	gga	att	cag	tgt	agg	aca	gtg	336	
Leu	Pro	Thr	Pro	Pro	His	Val	Thr	Leu	Gly	Ile	Gln	Cys	Arg	Thr	Val		
			100				105					110					
aag	gac	aaa	tca	cta	cac	ctg	agt	tct	gct	atc	ttg	gtt	ctt	tct	gtg	384	
Lys	Asp	Lys	Ser	Leu	His	Leu	Ser	Ser	Ala	Ile	Leu	Val	Leu	Ser	Val		
		115				120					125						
acc	aaa	cag	tct	gta	cgc	ccc	ctg	cag	agg	aac	cag	cat	ctg	gct	gac	432	
Thr	Lys	Gln	Ser	Val	Arg	Pro	Leu	Gln	Arg	Asn	Gln	His	Leu	Ala	Asp		
		130				135					140						
atc	tcc	aca	ggc	gca	gca	acc	acc	tgc	tgg	cca	gaa	gag	gta	aca	tta	480	
Ile	Ser	Thr	Gly	Ala	Ala	Thr	Thr	Cys	Trp	Pro	Glu	Glu	Val	Thr	Leu		
	145				150				155						160		
gta	gca	tat	tca	gtt	cac	acc	gaa	cgt	cat	tat	gaa	aat	cag	cag	aac	528	
Val	Ala	Tyr	Ser	Val	His	Thr	Glu	Arg	His	Tyr	Glu	Asn	Gln	Gln	Asn		
				165				170					175				
gga	aca	cca	gaa	agg	tcc	agt	gac	agg	ccc	cga	ggt	cac	agg	gca	ggg	576	
Gly	Thr	Pro	Glu	Arg	Ser	Ser	Asp	Arg	Pro	Arg	Gly	His	Arg	Ala	Gly		
			180				185						190				

624

657

<210> 206

<211> 218

<212> PRT

<213> Homo sapiens

<400> 206

Met Arg Asp Lys Ala Ala Pro Ala Trp Thr Val Leu Ala Leu Met Gln

1 5 10 15

Gly Val Gln Ala Lys Lys Glu Arg Pro Ser Trp Leu Arg Asp Ala Val

20 25 30

Leu Cys Ser Thr Thr Pro Val Pro Arg Ala Phe Pro Met Ala Lys His

35 40 45

Gln His Leu Pro Leu Phe Lys Ser Leu Ser Val Ala Gln Gln Lys Thr

50 55 60

Arg His Asp Thr Tyr Leu Arg Phe Asn Ile Leu Ile Leu Arg Leu Tyr

65 70 75 80

Asn Thr Gly Tyr Tyr Trp Gln His His Glu Thr Lys Lys Gln Lys Leu

85 90 95

Leu Pro Thr Pro Pro His Val Thr Leu Gly Ile Gln Cys Arg Thr Val

100 105 110

Lys Asp Lys Ser Leu His Leu Ser Ser Ala Ile Leu Val Leu Ser Val

115 120 125

Thr Lys Gln Ser Val Arg Pro Leu Gln Arg Asn Gln His Leu Ala Asp

130 135 140

Ile Ser Thr Gly Ala Ala Thr Thr Cys Trp Pro Glu Glu Val Thr Leu

145 150 155 160

Val Ala Tyr Ser Val His Thr Glu Arg His Tyr Glu Asn Gln Gln Asn

165 170 175

Gly Thr Pro Glu Arg Ser Ser Asp Arg Pro Arg Gly His Arg Ala Gly

180 185 190

Lys Leu Ala Asn Glu Leu Ile Ser Ala Asp Val His Val Cys Thr Phe

195 200 205

Tyr Pro Thr Pro Lys Pro Cys Ala Gly Phe

210 215

<220>
<221> CDS
<222> (1)...(354)

[illegible]

<210> 208
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 208

Met Ser Pro Gly Tyr Leu Leu Leu Leu Leu Leu Leu Glu Ser Pro Val
 1 5 10 15
 Ala Gly Arg Asn Cys Ala Thr Val Leu His Gln Asn Ser Cys His Leu
 20 25 30
 His Asp Asn Lys His Ala Leu Val Leu Pro Ala Trp Arg Gly Glu Glu
 35 40 45
 His Arg Glu Gly Ile Ser Tyr Cys Pro Pro Arg Arg Arg Thr Ser Asp
 50 55 60
 Arg Ile Ser Asn Ser Ile Gly Tyr Tyr Gly Asn Thr Phe Leu Leu Leu
 65 70 75 80
 Cys Thr Lys Leu Ala Asp Ile Ser Glu Gln Gly Gly Asp Trp Pro Ser
 85 90 95
 Gln Ile His Asn Ala Ala Glu Ala Glu Pro Ala Ala Ser Pro Leu Ser
 100 105 110
 Ala Asn Arg Asp Lys
 115

<210> 209
 <211> 693
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

<400> 209

atg ggc tcc ccg gcc acc gcc gcc acc ggg ctc ctc ctc ctg ctg ctg 48
 Met Gly Ser Pro Ala Thr Ala Ala Thr Gly Leu Leu Leu Leu Leu Leu
 1 5 10 15
 ctg ctg ctg ctg ctg ccg ccg cgg ctc ggc cgg gag aga aaa ggg ctg 96
 Leu Leu Leu Leu Leu Pro Pro Arg Leu Gly Arg Glu Arg Lys Gly Leu
 20 25 30
 agg gaa acg tgg tcc ctt ata tta ctt tca gcc gtg ggt tgt cct gag 144

Arg	Glu	Thr	Trp	Ser	Leu	Ile	Leu	Leu	Ser	Ala	Val	Gly	Cys	Pro	Glu	
		35					40					45				
ctg	ata	gca	cgc	gat	gat	cga	tgg	ttg	gac	ctt	aac	tgc	cgt	act	cat	192
Leu	Ile	Ala	Arg	Asp	Asp	Arg	Trp	Leu	Asp	Leu	Asn	Cys	Arg	Thr	His	
	50					55					60					
agt	gga	gac	act	atc	gca	tac	ccg	ttg	tcg	tgt	tcg	act	aat	ccc	gtt	240
Ser	Gly	Asp	Thr	Ile	Ala	Tyr	Pro	Leu	Ser	Cys	Ser	Thr	Asn	Pro	Val	
	65				70					75					80	
cgc	ggc	ggc	ctt	gtc	aac	aac	gtg	ccc	ttt	ggt	cct	cca	tca	cga	atg	288
Arg	Gly	Gly	Leu	Val	Asn	Asn	Val	Pro	Phe	Gly	Pro	Pro	Ser	Arg	Met	
				85				90						95		
tgc	agt	cat	tcg	atg	gct	gag	ggc	aag	atc	aca	cac	ttt	gtc	gtt	tct	336
Cys	Ser	His	Ser	Met	Ala	Glu	Gly	Lys	Ile	Thr	His	Phe	Val	Val	Ser	
			100					105					110			
tct	act	ttg	gtg	gat	gtg	cct	cag	tgc	ccg	cat	ggt	gca	ctc	ctt	gca	384
Ser	Thr	Leu	Val	Asp	Val	Pro	Gln	Cys	Pro	His	Gly	Ala	Leu	Leu	Ala	
			115				120					125				
ggt	ctc	cta	ctg	tgc	ctc	ccc	aag	gcc	act	gga	aga	acc	caa	act	gcc	432
Gly	Leu	Leu	Leu	Cys	Leu	Pro	Lys	Ala	Thr	Gly	Arg	Thr	Gln	Thr	Ala	
	130					135					140					
atc	gga	ttt	cag	agt	gtc	ggc	gtc	tgc	gta	aga	tta	cgc	tcc	att	acc	480
Ile	Gly	Phe	Gln	Ser	Val	Gly	Val	Cys	Val	Arg	Leu	Arg	Ser	Ile	Thr	
	145				150					155					160	
agt	agt	tgg	caa	gtt	cat	acg	ggc	cgc	cat	tgg	cac	gcc	atg	gag	ggt	528
Ser	Ser	Trp	Gln	Val	His	Thr	Gly	Arg	His	Trp	His	Ala	Met	Glu	Gly	
			165						170					175		
tac	tac	aga	gat	aat	cct	ggc	tct	aaa	tca	tcg	gtg	acg	ggg	aca	gtc	576
Tyr	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Lys	Ser	Ser	Val	Thr	Gly	Thr	Val	
			180					185					190			
tac	gac	atg	aca	tcc	tcc	aga	aaa	tcc	acc	gtg	ttg	gta	aag	gtg	ctc	624
Tyr	Asp	Met	Thr	Ser	Ser	Arg	Lys	Ser	Thr	Val	Leu	Val	Lys	Val	Leu	
		195					200					205				

672

693

 $\langle 400 \rangle$ 210

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<210> 211
<211> 307
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(307)

<400> 211

cca tgc ctc agc cag cga ctg agt gtg aca agg att ctc agt cct gtt 96
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
20 25 30

cct ggg aga tgt gag att cct ttg ctg gca aac ttc agc ttg aat att 144
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
35 40 45

ccc cag gtt agc caa ttc cca gag ata ata caa caa ctt gct aca cta 192
Pro Gln Val Ser Gln Phe Pro Glu Ile Ile Gln Gln Leu Ala Thr Leu
50 55 60

gca tgc ttt tca ggt tca aat cta cca att caa agc cct tac acc caa 240
Ala Cys Phe Ser Gly Ser Asn Leu Pro Ile Gln Ser Pro Tyr Thr Gln
65 70 75 80

cca cct act tta tct ggc tct tgc act ctg ggt cac tat cca ctt gcc 288
Pro Pro Thr Leu Ser Gly Ser Cys Thr Leu Gly His Tyr Pro Leu Ala
85 90 95

cta atc acc tca gga cca g 307
Leu Ile Thr Ser Gly Pro
100

<210> 212

<211> 102
 <212> PRT
 <213> Homo sapiens

<400> 212

Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
 1 5 10 15
 Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
 20 25 30
 Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
 35 40 45
 Pro Gln Val Ser Gln Phe Pro Glu Ile Ile Gln Gln Leu Ala Thr Leu
 50 55 60
 Ala Cys Phe Ser Gly Ser Asn Leu Pro Ile Gln Ser Pro Tyr Thr Gln
 65 70 75 80
 Pro Pro Thr Leu Ser Gly Ser Cys Thr Leu Gly His Tyr Pro Leu Ala
 85 90 95
 Leu Ile Thr Ser Gly Pro
 100

<210> 213
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(615)

<400> 213

atg tca cct cca agc acc tcc tgg ggt tgc ctg tcc tct ctc ctc ttc 48
 Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1 5 10 15
 ctg ctg agc ccc tgg gtc caa gga cct ccc acc ttc aaa aaa gta aaa 96
 Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
 20 25 30
 aca gca cag ccc aga ccc agg ggt aaa att cat gtc atc act tct tcc 144
 Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
 35 40 45
 tgg gcc agc acc caa ata cct cct gag cca cag gaa cac gat gcc tct 192

<210>	214
<211>	204
<212>	PRT

215

<213> Homo sapiens

<400> 214

Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
1 5 10 15
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
20 25 30
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
35 40 45
Trp Ala Ser Thr Gln Ile Pro Pro Glu Pro Gln Glu His Asp Ala Ser
50 55 60
Val Ala Leu Thr Ala Thr Ala Asp Cys Pro Gly Arg Gly Leu Gln Gly
65 70 75 80
Thr Ala Gln Glu Gly Gly Cys Ser Ser Ala Arg Phe Gln Ile Gln Gln
85 90 95
Asp Val His Asp Leu Pro Ala Asp Thr Asn Gly Gln Asn Val Thr Ala
100 105 110
Val Cys Phe Pro His Leu Tyr Gly Gly Tyr Pro Arg Ser Pro Pro Val
115 120 125
Thr Asp Cys Met Gln Ile Ser Val Ser Glu Phe Gly Pro Ser Thr Phe
130 135 140
Asn Leu Gly His Val Gly Pro Pro Ser Phe His Asp Lys Gln Pro Lys
145 150 155 160
Gln Gly Ser Tyr Val Met Cys Val Arg Trp His Asp Ser His Val Pro
165 170 175
Gln Leu Glu Leu Lys Leu His Pro Asp Ser Lys Ala Thr Leu Leu Ser
180 185 190
Leu His Asn Gln Cys Ser Glu His Ser Leu Gln Leu
195 200

<210> 215

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(483)

<400> 215

atg cct gat gtc tgg ggt cca gct gct gct gcc agt gct gcc tct tct
Met Pro Asp Val Trp Gly Pro Ala Ala Ala Ala Ser Ala Ala Ser Ser
1 5 10 15

48

gct gcc aac ccc act ctt ttc atc ctc ctg ctg ctt cca cca aca ttt	96
Ala Ala Asn Pro Thr Leu Phe Ile Leu Leu Leu Leu Pro Pro Thr Phe	
20 25 30	
ctg ctg cca tcg cca aaa tta cag atg ctg cca gca ctg cag ctt tgc	144
Leu Leu Pro Ser Pro Lys Leu Gln Met Leu Pro Ala Leu Gln Leu Cys	
35 40 45	
ttc ccc cct gct gtc ttg ttg ctg cat tgc cat ggc atc agg caa ggg	192
Phe Pro Pro Ala Val Leu Leu Leu His Cys His Gly Ile Arg Gln Gly	
50 55 60	
ttc agg ggc cta ggc aaa tgg act gtg gca ctt gta tgt ctc cct cct	240
Phe Arg Gly Leu Gly Lys Trp Thr Val Ala Leu Val Cys Leu Pro Pro	
65 70 75 80	
gga aaa tgc agg cta tcc aat aaa ggg gag aga gga aca ggg cag agc	288
Gly Lys Cys Arg Leu Ser Asn Lys Gly Glu Arg Gly Thr Gly Gln Ser	
85 90 95	
act ata aaa ggc aaa cac cgt ggt gaa att tgc agc acc atc cgg ctg	336
Thr Ile Lys Gly Lys His Arg Gly Glu Ile Cys Ser Thr Ile Arg Leu	
100 105 110	
cca aat tta gca tcc agg tca ctg gtg cca cgg aaa gcg ttg cca ctg	384
Pro Asn Leu Ala Ser Arg Ser Leu Val Pro Arg Lys Ala Leu Pro Leu	
115 120 125	
atg ctt gtg ccg gga aag gca cct ctc ctc tgc ttc agt gtc cat gct	432
Met Leu Val Pro Gly Lys Ala Pro Leu Leu Cys Phe Ser Val His Ala	
130 135 140	
aag gga aac cta atg cct cac act gac aaa aat gca ccc agt gga tct	480
Lys Gly Asn Leu Met Pro His Thr Asp Lys Asn Ala Pro Ser Gly Ser	
145 150 155 160	
taa	483
*	

<211> 160
 <212> PRT
 <213> Homo sapiens

<400> 216

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Met Pro Asp Val Trp Gly Pro Ala Ala Ala Ala Ser Ala Ala Ser Ser
 1           5           10           15
Ala Ala Asn Pro Thr Leu Phe Ile Leu Leu Leu Leu Pro Pro Thr Phe
          20           25           30
Leu Leu Pro Ser Pro Lys Leu Gln Met Leu Pro Ala Leu Gln Leu Cys
          35           40           45
Phe Pro Pro Ala Val Leu Leu Leu His Cys His Gly Ile Arg Gln Gly
          50           55           60
Phe Arg Gly Leu Gly Lys Trp Thr Val Ala Leu Val Cys Leu Pro Pro
65           70           75           80
Gly Lys Cys Arg Leu Ser Asn Lys Gly Glu Arg Gly Thr Gly Gln Ser
          85           90           95
Thr Ile Lys Gly Lys His Arg Gly Glu Ile Cys Ser Thr Ile Arg Leu
          100          105          110
Pro Asn Leu Ala Ser Arg Ser Leu Val Pro Arg Lys Ala Leu Pro Leu
          115          120          125
Met Leu Val Pro Gly Lys Ala Pro Leu Leu Cys Phe Ser Val His Ala
          130          135          140
Lys Gly Asn Leu Met Pro His Thr Asp Lys Asn Ala Pro Ser Gly Ser
145           150           155           160

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<210> 217
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(240)

<400> 217

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atg acc aac aga ttc ttg ctc ctg tta tct tct ttc cag cag gtc tat      48
Met Thr Asn Arg Phe Leu Leu Leu Leu Ser Ser Phe Gln Gln Val Tyr
 1           5           10           15

ggg gac cgt aaa act gtt aaa gac ttt tgt tca ggc tcc ctc aac agt      96
Gly Asp Arg Lys Thr Val Lys Asp Phe Cys Ser Gly Ser Leu Asn Ser
          20           25           30

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gaa atg atg tcc cct ccc ccc aca tct gtg ttg atc tac ttt act ctc 144
 Glu Met Met Ser Pro Pro Pro Thr Ser Val Leu Ile Tyr Phe Thr Leu
 35 40 45

aat cgg tgc atc ctt cca cat ggg aaa atg gaa tat agg gca tca gtg 192
 Asn Arg Cys Ile Leu Pro His Gly Lys Met Glu Tyr Arg Ala Ser Val
 50 55 60

cat tct ctg gtt gta gct tct tgc tta tat cat caa gga aat gat tag 240
 His Ser Leu Val Val Ala Ser Cys Leu Tyr His Gln Gly Asn Asp *
 65 70 75

<210> 218

<211> 79

<212> PRT

<213> Homo sapiens

<400> 218

Met Thr Asn Arg Phe Leu Leu Leu Leu Ser Ser Phe Gln Gln Val Tyr
 1 5 10 15
 Gly Asp Arg Lys Thr Val Lys Asp Phe Cys Ser Gly Ser Leu Asn Ser
 20 25 30
 Glu Met Met Ser Pro Pro Pro Thr Ser Val Leu Ile Tyr Phe Thr Leu
 35 40 45
 Asn Arg Cys Ile Leu Pro His Gly Lys Met Glu Tyr Arg Ala Ser Val
 50 55 60
 His Ser Leu Val Val Ala Ser Cys Leu Tyr His Gln Gly Asn Asp
 65 70 75

<210> 219

<211> 681

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(681)

<400> 219

atg aat ctg cag cac cag ccc ctg cca gtc tcc cac agc cag ggt ggc 48
 Met Asn Leu Gln His Gln Pro Leu Pro Val Ser His Ser Gln Gly Gly

1	5	10	15	
caa gcc ctc agg gct ctg cag gac aat cct cgg cgt ctg ctg ctg ctg				96
Gln Ala Leu Arg Ala Leu Gln Asp Asn Pro Arg Arg Leu Leu Leu Leu				
20	25	30		
ctg ctg ctg ctg gaa cct tct cag ggt gtc ctc tgc tgg cag gca ggc				144
Leu Leu Leu Leu Glu Pro Ser Gln Gly Val Leu Cys Trp Gln Ala Gly				
35	40	45		
ttc gca cac agc ctc tgc cag ggc tgt gca cag cag gca gca cca ggc				192
Phe Ala His Ser Leu Cys Gln Gly Cys Ala Gln Gln Ala Ala Pro Gly				
50	55	60		
cac agc att gac tgg cta ttt gtg caa cgc tgg ttg aag acg cca gtg				240
His Ser Ile Asp Trp Leu Phe Val Gln Arg Trp Leu Lys Thr Pro Val				
65	70	75	80	
acc tgg aaa agg gcc caa gcc agg ccg cgg ccg cgg ctc ctc gac tcc				288
Thr Trp Lys Arg Ala Gln Ala Arg Pro Arg Pro Arg Leu Leu Asp Ser				
85	90	95		
tcc ggt cac ctg gcc cca gcc tgg gac cgc tcc cgc ctc cag ccg ctg				336
Ser Gly His Leu Ala Pro Ala Trp Asp Arg Ser Arg Leu Gln Pro Leu				
100	105	110		
gaa agc atc tcc agg ctg gtg gcg cgg act ttc atg gaa aca tca cct				384
Glu Ser Ile Ser Arg Leu Val Ala Arg Thr Phe Met Glu Thr Ser Pro				
115	120	125		
ctc ttc aaa gga tcc ttg gat ccc cca aaa gag aac acc agc tct ggg				432
Leu Phe Lys Gly Ser Leu Asp Pro Pro Lys Glu Asn Thr Ser Ser Gly				
130	135	140		
atc gcc agg ccc tgg ctc agc tct cca ccc tgt aat gaa atg gcc agc				480
Ile Ala Arg Pro Trp Leu Ser Ser Pro Pro Cys Asn Glu Met Ala Ser				
145	150	155	160	
tat ctg gga cat tac tgt agc ctc ctc gcc atc aga act gtc act ccc				528
Tyr Leu Gly His Tyr Cys Ser Leu Leu Ala Ile Arg Thr Val Thr Pro				
165	170	175		
gct gcc atc atc ctc tcc ttc agc acc atc tcc att ctc atc act cgc				576

Ala Ala Ile Ile Leu Ser Phe Ser Thr Ile Ser Ile Leu Ile Thr Arg
 180 185 190

atc acc acc acc tca cac aga acc atc tgc atc ctt ctg ctc acc cag 624
 Ile Thr Thr Thr Ser His Arg Thr Ile Cys Ile Leu Leu Leu Thr Gln
 195 200 205

tgg acc ctc ttc tcc ctg tac cca ggg agg aac cct atc agc att tgc 672
 Trp Thr Leu Phe Ser Leu Tyr Pro Gly Arg Asn Pro Ile Ser Ile Cys
 210 215 220

tgc ctt tga 681
 Cys Leu *
 225

<210> 220
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 220

Met Asn Leu Gln His Gln Pro Leu Pro Val Ser His Ser Gln Gly Gly
 1 5 10 15
 Gln Ala Leu Arg Ala Leu Gln Asp Asn Pro Arg Arg Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Glu Pro Ser Gln Gly Val Leu Cys Trp Gln Ala Gly
 35 40 45
 Phe Ala His Ser Leu Cys Gln Gly Cys Ala Gln Gln Ala Ala Pro Gly
 50 55 60
 His Ser Ile Asp Trp Leu Phe Val Gln Arg Trp Leu Lys Thr Pro Val
 65 70 75 80
 Thr Trp Lys Arg Ala Gln Ala Arg Pro Arg Pro Arg Leu Leu Asp Ser
 85 90 95
 Ser Gly His Leu Ala Pro Ala Trp Asp Arg Ser Arg Leu Gln Pro Leu
 100 105 110
 Glu Ser Ile Ser Arg Leu Val Ala Arg Thr Phe Met Glu Thr Ser Pro
 115 120 125
 Leu Phe Lys Gly Ser Leu Asp Pro Pro Lys Glu Asn Thr Ser Ser Gly
 130 135 140
 Ile Ala Arg Pro Trp Leu Ser Ser Pro Pro Cys Asn Glu Met Ala Ser
 145 150 155 160
 Tyr Leu Gly His Tyr Cys Ser Leu Leu Ala Ile Arg Thr Val Thr Pro

165 170 175
 Ala Ala Ile Ile Leu Ser Phe Ser Thr Ile Ser Ile Leu Ile Thr Arg
 180 185 190
 Ile Thr Thr Thr Ser His Arg Thr Ile Cys Ile Leu Leu Leu Thr Gln
 195 200 205
 Trp Thr Leu Phe Ser Leu Tyr Pro Gly Arg Asn Pro Ile Ser Ile Cys
 210 215 220
 Cys Leu
 225

<210> 221
 <211> 441
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(441)

<400> 221
 atg aca agg ctt ttt tgg ctg tgt gtg tcc agc tgt tcc atg cca gga 48
 Met Thr Arg Leu Phe Trp Leu Cys Val Ser Ser Cys Ser Met Pro Gly
 1 5 10 15
 gga gga gga gtt aca tgc tgg aag ctt gca gat agc ctg ggg ctg ctg 96
 Gly Gly Gly Val Thr Cys Trp Lys Leu Ala Asp Ser Leu Gly Leu Leu
 20 25 30
 ctc gcc ttg ctg cgg ttg gtg gca gct acc gag act acc tcg cac cag 144
 Leu Ala Leu Leu Arg Leu Val Ala Ala Thr Glu Thr Thr Ser His Gln
 35 40 45
 agc ggc ctg gcc ggg cag gcc ccg cag cgc tcc tac tcc ctc ttc ccg 192
 Ser Gly Leu Ala Gly Gln Ala Pro Gln Arg Ser Tyr Ser Leu Phe Pro
 50 55 60
 gcc cct gga ctt gcg gct gct gcc aca act agc gca gat gtc act ata 240
 Ala Pro Gly Leu Ala Ala Ala Ala Thr Thr Ser Ala Asp Val Thr Ile
 65 70 75 80
 acc atc gct gct gtt gcc ctc aat gca ctg gcc cac cct aca aag ctc 288
 Thr Ile Ala Ala Val Ala Leu Asn Ala Leu Ala His Pro Thr Lys Leu
 85 90 95

ggc cgt cct cct acc gct ctg gtg cga ggt agt ctc ggt agc tgc cac 384
Gly Arg Pro Pro Thr Ala Leu Val Arg Gly Ser Leu Gly Ser Cys His
115 120 125

agc atg taa 441
Ser Met *
145

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<210> 222
<211> 146
<212> PRT
<213> Homo sapiens
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<400> 222

[illegible]

145

<210> 223
 <211> 576
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(576)

<400> 223

atg aag gca tcc tgg gtg cac ctg gcg ctc tgc ctg gcc cac agc gca	48
Met Lys Ala Ser Trp Val His Leu Ala Leu Cys Leu Ala His Ser Ala	
1 5 10 15	
cg t ggg gca gac ctc agg ccg cag tca cgg ggc tgc tca ggt gct gcg	96
Arg Gly Ala Asp Leu Arg Pro Gln Ser Arg Gly Cys Ser Gly Ala Ala	
20 25 30	
atg gga gaa gag cca gga agt gag tct cca ccc agt gcc gct cag tca	144
Met Gly Glu Glu Pro Gly Ser Glu Ser Pro Pro Ser Ala Ala Gln Ser	
35 40 45	
cg g gac cca gaa ctc act gaa ccg ccc acg tta atg acg cgc agt tcg	192
Arg Asp Pro Glu Leu Thr Glu Pro Pro Thr Leu Met Thr Arg Ser Ser	
50 55 60	
ccg tgt gcc aat gac gcc tca atc aag ctg cta aac gaa ggc cgg agc	240
Pro Cys Ala Asn Asp Ala Ser Ile Lys Leu Leu Asn Glu Gly Arg Ser	
65 70 75 80	
agc cct gcc tgt ggg gct gta atg ttt tct gca gcc ttg atg agc cgc	288
Ser Pro Ala Cys Gly Ala Val Met Phe Ser Ala Ala Leu Met Ser Arg	
85 90 95	
cct ggg ctg ttt caa agg gaa cgc agc agt ctc ctc ttg act tcc gca	336
Pro Gly Leu Phe Gln Arg Glu Arg Ser Ser Leu Leu Leu Thr Ser Ala	
100 105 110	
gtg gcc gta ttc ctg ggc cgt gcg gta aac agg gag tat cta ggc tcg	384
Val Ala Val Phe Leu Gly Arg Ala Val Asn Arg Glu Tyr Leu Gly Ser	
115 120 125	

gat ggt tac aga cgg ctt tcc ccg tgg gcg gcg tcc cgt ggg ccc tat 432
 Asp Gly Tyr Arg Arg Leu Ser Pro Trp Ala Ala Ser Arg Gly Pro Tyr
 130 135 140

 gca agc tgc gca ggc cgc cct ggg ctc tgc cgc gag tgc gtg ggc ggc 480
 Ala Ser Cys Ala Gly Arg Pro Gly Leu Cys Arg Glu Cys Val Gly Gly
 145 150 155 160

 agg acg gtg cat ccc ggg cct cca ccg gtc aaa tgc tcc aca ctg acc 528
 Arg Thr Val His Pro Gly Pro Pro Pro Val Lys Cys Ser Thr Leu Thr
 165 170 175

 acc gca gca ccc ccc cgc tct ccc ggg caa att cta aag ctt ccc tag 576
 Thr Ala Ala Pro Pro Arg Ser Pro Gly Gln Ile Leu Lys Leu Pro *
 180 185 190

<210> 224

<211> 191

<212> PRT

<213> Homo sapiens

<400> 224

Met Lys Ala Ser Trp Val His Leu Ala Leu Cys Leu Ala His Ser Ala
 1 5 10 15
 Arg Gly Ala Asp Leu Arg Pro Gln Ser Arg Gly Cys Ser Gly Ala Ala
 20 25 30
 Met Gly Glu Glu Pro Gly Ser Glu Ser Pro Pro Ser Ala Ala Gln Ser
 35 40 45
 Arg Asp Pro Glu Leu Thr Glu Pro Pro Thr Leu Met Thr Arg Ser Ser
 50 55 60
 Pro Cys Ala Asn Asp Ala Ser Ile Lys Leu Leu Asn Glu Gly Arg Ser
 65 70 75 80
 Ser Pro Ala Cys Gly Ala Val Met Phe Ser Ala Ala Leu Met Ser Arg
 85 90 95
 Pro Gly Leu Phe Gln Arg Glu Arg Ser Ser Leu Leu Leu Thr Ser Ala
 100 105 110
 Val Ala Val Phe Leu Gly Arg Ala Val Asn Arg Glu Tyr Leu Gly Ser
 115 120 125
 Asp Gly Tyr Arg Arg Leu Ser Pro Trp Ala Ala Ser Arg Gly Pro Tyr
 130 135 140
 Ala Ser Cys Ala Gly Arg Pro Gly Leu Cys Arg Glu Cys Val Gly Gly

145 150 155 160
 Arg Thr Val His Pro Gly Pro Pro Pro Val Lys Cys Ser Thr Leu Thr
 165 170 175
 Thr Ala Ala Pro Pro Arg Ser Pro Gly Gln Ile Leu Lys Leu Pro
 180 185 190

<210> 225

<211> 870

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(870)

<400> 225

atg aac agt gct ttc ttg ttg ctt ttt gct tgt atc ctc aca gcc ctt 48
 Met Asn Ser Ala Phe Leu Leu Leu Phe Ala Cys Ile Leu Thr Ala Leu
 1 5 10 15

ctt tcc gct tcc tgc ctc ttt aag ggc ata gat aat aca gaa gca gaa 96
 Leu Ser Ala Ser Cys Leu Phe Lys Gly Ile Asp Asn Thr Glu Ala Glu
 20 25 30

aag cga gac ccc cag gaa ctc gtg gcc tcc ttt tct gaa aga gtt cgg 144
 Lys Arg Asp Pro Gln Glu Leu Val Ala Ser Phe Ser Glu Arg Val Arg
 35 40 45

aac atg tcg cct gat gaa atc aag atc ccg cca gaa ccc cct ggc aga 192
 Asn Met Ser Pro Asp Glu Ile Lys Ile Pro Pro Glu Pro Pro Gly Arg
 50 55 60

tgt tca aat cac ttg caa aat cac gtc acc ctc cgt gcc aga caa cca 240
 Cys Ser Asn His Leu Gln Asn His Val Thr Leu Arg Ala Arg Gln Pro
 65 70 75 80

gac aac aag ctc cag cct cta aca ggt cca tct ccc tgg gag agt gga 288
 Asp Asn Lys Leu Gln Pro Leu Thr Gly Pro Ser Pro Trp Glu Ser Gly
 85 90 95

ggg cca tca gga agc ttg ctt aga gca gct gag ctg gat tta aaa gtt 336
 Gly Pro Ser Gly Ser Leu Leu Arg Ala Ala Glu Leu Asp Leu Lys Val
 100 105 110

gtg aag gtt ttg tgt cag ccc cag gag ctg gat ggt tca ggt ccc atg	384
Val Lys Val Leu Cys Gln Pro Gln Glu Leu Asp Gly Ser Gly Pro Met	
115 120 125	
cag gga cgt gga ctt gtg cct gct cag cgc cgg cac tgt tct ttc agc	432
Gln Gly Arg Gly Leu Val Pro Ala Gln Arg Arg His Cys Ser Phe Ser	
130 135 140	
atc tac gag aag ctg atc cag ttc tgt gcc att gac gag ctt ggc acc	480
Ile Tyr Glu Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr	
145 150 155 160	
aac tac cca aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc	528
Asn Tyr Pro Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser	
165 170 175	
tac tat gag gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg	576
Tyr Tyr Glu Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu	
180 185 190	
gaa aag gcc aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc	624
Glu Lys Ala Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr	
195 200 205	
aaa aaa ggc acc acg acc aac gcc acg tcc acc acc act acc act gcc	672
Lys Lys Gly Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Ala	
210 215 220	
agc aca gct gtt gca gat gct cag aag aga aag agc aag tgg gat tcg	720
Ser Thr Ala Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser	
225 230 235 240	
gct atc cca gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca	768
Ala Ile Pro Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr	
245 250 255	
gcc acc ctg cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc	816
Ala Thr Leu Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser	
260 265 270	
aag acc acc gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag	864
Lys Thr Thr Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys	

275

280

285

cag tga

Gln *

870

<210> 226

<211> 289

<212> PRT

<213> Homo sapiens

<400> 226

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Met Asn Ser Ala Phe Leu Leu Leu Phe Ala Cys Ile Leu Thr Ala Leu
 1          5          10          15
Leu Ser Ala Ser Cys Leu Phe Lys Gly Ile Asp Asn Thr Glu Ala Glu
          20          25          30
Lys Arg Asp Pro Gln Glu Leu Val Ala Ser Phe Ser Glu Arg Val Arg
          35          40          45
Asn Met Ser Pro Asp Glu Ile Lys Ile Pro Pro Glu Pro Pro Gly Arg
 50          55          60
Cys Ser Asn His Leu Gln Asn His Val Thr Leu Arg Ala Arg Gln Pro
65          70          75          80
Asp Asn Lys Leu Gln Pro Leu Thr Gly Pro Ser Pro Trp Glu Ser Gly
          85          90          95
Gly Pro Ser Gly Ser Leu Leu Arg Ala Ala Glu Leu Asp Leu Lys Val
          100          105          110
Val Lys Val Leu Cys Gln Pro Gln Glu Leu Asp Gly Ser Gly Pro Met
          115          120          125
Gln Gly Arg Gly Leu Val Pro Ala Gln Arg Arg His Cys Ser Phe Ser
          130          135          140
Ile Tyr Glu Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr
          145          150          155          160
Asn Tyr Pro Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser
          165          170          175
Tyr Tyr Glu Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu
          180          185          190
Glu Lys Ala Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr
          195          200          205
Lys Lys Gly Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Ala
          210          215          220
Ser Thr Ala Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser
          225          230          235          240

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Ala Ile Pro Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr
 245 250 255
 Ala Thr Leu Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser
 260 265 270
 Lys Thr Thr Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys
 275 280 285
 Gln

<210> 227
 <211> 822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(822)

<400> 227
 atg cgc ctt ccc ggg gta ccc ctg gcg cgc cct gcg ctg ctg ctg ctg 48
 Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
 1 5 10 15

 ctg ccg ctg ctc gcg ccg ctg ctg gga acg ggt gcg ccg gcc gag ctg 96
 Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
 20 25 30

 cgg gtc cgc gtg cgg ctg ccg gac ggc cag gtg acc gag gag agc ctg 144
 Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
 35 40 45

 cag gcg gac agc gac gcg gac agc atc agc ctc gag ctg cgc aag ccc 192
 Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
 50 55 60

 gac ggc acc ctc gtc tcc ttc acc gcc gac ttc aag aag gat gtg aag 240
 Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
 65 70 75 80

 gtc ttc cgg gcc ctg atc ctg ggg gag ctg gag aag ggg cag agt cag 288
 Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
 85 90 95

ttc	cag	gcc	ctc	tgc	ttt	gtc	acc	cag	ctg	cag	cac	aat	gag	atc	atc	336
Phe	Gln	Ala	Leu	Cys	Phe	Val	Thr	Gln	Leu	Gln	His	Asn	Glu	Ile	Ile	
		100						105					110			
ccc	agt	gag	gcc	atg	gcc	aag	ctc	cgg	cag	aaa	aat	ccc	cgg	gca	gtg	384
Pro	Ser	Glu	Ala	Met	Ala	Lys	Leu	Arg	Gln	Lys	Asn	Pro	Arg	Ala	Val	
		115					120					125				
cgg	cag	gcg	gag	gag	gtt	cgg	ggt	ctg	gag	cat	ctg	cac	atg	gat	gtc	432
Arg	Gln	Ala	Glu	Glu	Val	Arg	Gly	Leu	Glu	His	Leu	His	Met	Asp	Val	
	130					135					140					
gct	gtc	aac	ttc	agc	cag	ggg	gcc	ctg	ctg	agc	ccc	cat	ctc	cac	aac	480
Ala	Val	Asn	Phe	Ser	Gln	Gly	Ala	Leu	Leu	Ser	Pro	His	Leu	His	Asn	
145					150					155					160	
gtg	tgt	gcc	gag	gcc	gtg	gat	gcc	atc	tac	acc	cgc	cag	gag	gat	gtc	528
Val	Cys	Ala	Glu	Ala	Val	Asp	Ala	Ile	Tyr	Thr	Arg	Gln	Glu	Asp	Val	
				165					170					175		
cgg	ttc	tgg	ctg	gag	caa	ggt	gtg	gac	agt	tct	gtg	ttc	gag	gct	ctg	576
Arg	Phe	Trp	Leu	Glu	Gln	Gly	Val	Asp	Ser	Ser	Val	Phe	Glu	Ala	Leu	
			180					185					190			
ccc	aag	gcc	tca	gag	cag	gcg	gag	ctg	cct	cgc	tgc	agg	cag	gtg	ggg	624
Pro	Lys	Ala	Ser	Glu	Gln	Ala	Glu	Leu	Pro	Arg	Cys	Arg	Gln	Val	Gly	
		195					200					205				
gac	cgc	ggg	aag	ccc	tgc	gtc	tgc	cac	tat	ggc	ctg	agc	ctg	gcc	tgg	672
Asp	Arg	Gly	Lys	Pro	Cys	Val	Cys	His	Tyr	Gly	Leu	Ser	Leu	Ala	Trp	
	210					215					220					
tac	ccc	tgc	atg	ctc	aag	tac	tgc	cac	agc	cgc	gac	cgg	ccc	acg	ccc	720
Tyr	Pro	Cys	Met	Leu	Lys	Tyr	Cys	His	Ser	Arg	Asp	Arg	Pro	Thr	Pro	
225					230					235					240	
tac	aag	tgt	ggc	atc	cgc	agc	tgc	cag	aag	agc	tac	agc	ttt	gac	ttc	768
Tyr	Lys	Cys	Gly	Ile	Arg	Ser	Cys	Gln	Lys	Ser	Tyr	Ser	Phe	Asp	Phe	
				245					250					255		
tac	gtg	ccc	cag	agg	cag	ctg	tgt	ctc	tgg	gat	gag	gat	ccc	tac	cca	816
Tyr	Val	Pro	Gln	Arg	Gln	Leu	Cys	Leu	Trp	Asp	Glu	Asp	Pro	Tyr	Pro	
			260					265					270			

822

<400> 228															
Met	Arg	Leu	Pro	Gly	Val	Pro	Leu	Ala	Arg	Pro	Ala	Leu	Leu	Leu	Leu
1				5					10					15	
Leu	Pro	Leu	Leu	Ala	Pro	Leu	Leu	Gly	Thr	Gly	Ala	Pro	Ala	Glu	Leu
			20					25					30		
Arg	Val	Arg	Val	Arg	Leu	Pro	Asp	Gly	Gln	Val	Thr	Glu	Glu	Ser	Leu
		35					40						45		
Gln	Ala	Asp	Ser	Asp	Ala	Asp	Ser	Ile	Ser	Leu	Glu	Leu	Arg	Lys	Pro
	50					55					60				
Asp	Gly	Thr	Leu	Val	Ser	Phe	Thr	Ala	Asp	Phe	Lys	Lys	Asp	Val	Lys
65					70					75					80
Val	Phe	Arg	Ala	Leu	Ile	Leu	Gly	Glu	Leu	Glu	Lys	Gly	Gln	Ser	Gln
				85					90						95
Phe	Gln	Ala	Leu	Cys	Phe	Val	Thr	Gln	Leu	Gln	His	Asn	Glu	Ile	Ile
			100					105					110		
Pro	Ser	Glu	Ala	Met	Ala	Lys	Leu	Arg	Gln	Lys	Asn	Pro	Arg	Ala	Val
		115					120					125			
Arg	Gln	Ala	Glu	Glu	Val	Arg	Gly	Leu	Glu	His	Leu	His	Met	Asp	Val
	130					135					140				
Ala	Val	Asn	Phe	Ser	Gln	Gly	Ala	Leu	Leu	Ser	Pro	His	Leu	His	Asn
145					150					155					160
Val	Cys	Ala	Glu	Ala	Val	Asp	Ala	Ile	Tyr	Thr	Arg	Gln	Glu	Asp	Val
				165					170					175	
Arg	Phe	Trp	Leu	Glu	Gln	Gly	Val	Asp	Ser	Ser	Val	Phe	Glu	Ala	Leu
			180					185					190		
Pro	Lys	Ala	Ser	Glu	Gln	Ala	Glu	Leu	Pro	Arg	Cys	Arg	Gln	Val	Gly
		195					200					205			
Asp	Arg	Gly	Lys	Pro	Cys	Val	Cys	His	Tyr	Gly	Leu	Ser	Leu	Ala	Trp
	210					215					220				
Tyr	Pro	Cys	Met	Leu	Lys	Tyr	Cys	His	Ser	Arg	Asp	Arg	Pro	Thr	Pro
225					230					235					240
Tyr	Lys	Cys	Gly	Ile	Arg	Ser	Cys	Gln	Lys	Ser	Tyr	Ser	Phe	Asp	Phe

Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
 245 250 255
 260 265 270

Gly

<210> 229
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(453)

<400> 229

atg gtg gta ttt acc ttg ctg ctg gtg ctg ctg ttg ttg ctg ctg cta 48
 Met Val Val Phe Thr Leu Leu Leu Val Leu Leu Leu Leu Leu Leu
 1 5 10 15

aca gct cta tgt aag gct ctg agt caa agc ctt ccc tat acc ctc tac 96
 Thr Ala Leu Cys Lys Ala Leu Ser Gln Ser Leu Pro Tyr Thr Leu Tyr
 20 25 30

agg cca cag tca tca cta tcc ttc ctc ctt atc act gat ata aaa aag 144
 Arg Pro Gln Ser Ser Leu Ser Phe Leu Leu Ile Thr Asp Ile Lys Lys
 35 40 45

att gat ata cag tat ttt ctc cca ttg aca ggt ggc aag tgc ctg cat 192
 Ile Asp Ile Gln Tyr Phe Leu Pro Leu Thr Gly Gly Lys Cys Leu His
 50 55 60

ctt cgc ttg aca gga cag agg gct ttc tgt atc ctg gag ttc ttg cct 240
 Leu Arg Leu Thr Gly Gln Arg Ala Phe Cys Ile Leu Glu Phe Leu Pro
 65 70 75 80

tgg tgt aat gga ata att gaa tca ctc gtg ggc ttg gag aat gag cgc 288
 Trp Cys Asn Gly Ile Ile Glu Ser Leu Val Gly Leu Glu Asn Glu Arg
 85 90 95

aag gtt ttg agt gga ggt agc tct cag cag atg ggg gaa gcc aga agg 336
 Lys Val Leu Ser Gly Gly Ser Ser Gln Gln Met Gly Glu Ala Arg Arg
 100 105 110

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$$\begin{array}{ll} \langle 210 \rangle & 231 \\ \langle 211 \rangle & 768 \end{array}$$

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(768)

<400> 231

atg cgc ccc cga gcc cca gcc tgc gcc gcc gcg gcg ctc ggg ctc tgc	48
Met Arg Pro Arg Ala Pro Ala Cys Ala Ala Ala Ala Leu Gly Leu Cys	
1 5 10 15	
agc ctt ctg ctg ctg ctc gcg ccc ggg cac gcg tgc ccc gcg ggc tgc	96
Ser Leu Leu Leu Leu Leu Ala Pro Gly His Ala Cys Pro Ala Gly Cys	
20 25 30	
gcc tgc acc gac ccg cac acc gtg gac tgc cgc gac cgc ggg ctg ccc	144
Ala Cys Thr Asp Pro His Thr Val Asp Cys Arg Asp Arg Gly Leu Pro	
35 40 45	
agc gtg cca gac cct ttc ccc ctg gac gtg cgc aag ctg ctg gtg gcc	192
Ser Val Pro Asp Pro Phe Pro Leu Asp Val Arg Lys Leu Leu Val Ala	
50 55 60	
ggc aac cgc atc cag cgg atc ccc gag gac ttc ttc atc ttc tac ggc	240
Gly Asn Arg Ile Gln Arg Ile Pro Glu Asp Phe Phe Ile Phe Tyr Gly	
65 70 75 80	
gac ctg gtc tac ctg gac ttc agg aac aac tcg ctg cgc tcg ctg gag	288
Asp Leu Val Tyr Leu Asp Phe Arg Asn Asn Ser Leu Arg Ser Leu Glu	
85 90 95	
gag ggc acg ttc agc ggc tcg gcc aag ctc gtg ttc ctc gac ctc agc	336
Glu Gly Thr Phe Ser Gly Ser Ala Lys Leu Val Phe Leu Asp Leu Ser	
100 105 110	
tac aac aac ttg acc cag ctg ggc gcc ggc gcc ttc cgc tcg gcc ggc	384
Tyr Asn Asn Leu Thr Gln Leu Gly Ala Gly Ala Phe Arg Ser Ala Gly	
115 120 125	
agg ctg gtg aag ctt agc ctg gct aac aac aac ctg gtg ggc gtg cac	432
Arg Leu Val Lys Leu Ser Leu Ala Asn Asn Asn Leu Val Gly Val His	
130 135 140	

gag gac gcc ttc gag acc ctg gag tcg ctg cag gtg ctg gag ctc aac 480
 Glu Asp Ala Phe Glu Thr Leu Glu Ser Leu Gln Val Leu Glu Leu Asn
 145 150 155 160

 gac aac aac ctg cgc agc ctc agc gtg gcc gcc ctg gcc gcg ctg ccc 528
 Asp Asn Asn Leu Arg Ser Leu Ser Val Ala Ala Leu Ala Ala Leu Pro
 165 170 175

 gcg ctg cgc tcc ctg cgt ctg gac ggg aac ccc tgg ctg tgc gac tgt 576
 Ala Leu Arg Ser Leu Arg Leu Asp Gly Asn Pro Trp Leu Cys Asp Cys
 180 185 190

 gac ttc gcc cac ctc ttc tcc tgg atc cag gag aac gca tcc aaa ctg 624
 Asp Phe Ala His Leu Phe Ser Trp Ile Gln Glu Asn Ala Ser Lys Leu
 195 200 205

 ccc aaa gga ctg gcg ggt gtg gat tac tta tgc gtc cct ggt aag cgg 672
 Pro Lys Gly Leu Ala Gly Val Asp Tyr Leu Cys Val Pro Gly Lys Arg
 210 215 220

 aat gca gcc tac tct atg gga aac ggc cgt att ctc agt acc gtg cac 720
 Asn Ala Ala Tyr Ser Met Gly Asn Gly Arg Ile Leu Ser Thr Val His
 225 230 235 240

 ggg gag tca gcc agt tcc aag ggc tct cca gca gct tcc cga gcc taa 768
 Gly Glu Ser Ala Ser Ser Lys Gly Ser Pro Ala Ala Ser Arg Ala *
 245 250 255

<210> 232

<211> 255

<212> PRT

<213> Homo sapiens

<400> 232

Met Arg Pro Arg Ala Pro Ala Cys Ala Ala Ala Ala Leu Gly Leu Cys
 1 5 10 15
 Ser Leu Leu Leu Leu Leu Ala Pro Gly His Ala Cys Pro Ala Gly Cys
 20 25 30
 Ala Cys Thr Asp Pro His Thr Val Asp Cys Arg Asp Arg Gly Leu Pro
 35 40 45
 Ser Val Pro Asp Pro Phe Pro Leu Asp Val Arg Lys Leu Leu Val Ala

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<210> 233
<211> 615
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(615)

<400> 233
atg tca cct cca agc acc tcc tgg ggt tgc ctg tcc tct ctc ctc ttc
Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
  1             5             10             15

ctg ctg agc ccc tgg gtc caa gga cct ccc acc ttc aaa aaa gta aaa
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
      20             25             30

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aca Thr	gca Ala	cag Gln	ccc Pro	aga Arg	ccc Pro	agg Arg	ggt Gly	aaa Lys	att Ile	cat His	gtc Val	atc Ile	act Thr	tct Ser	tcc Ser	144
		35				40						45				
tgg Trp	gcc Ala	agc Ser	acc Thr	caa Gln	ata Ile	cct Pro	cct Pro	gag Glu	cca Pro	cag Gln	gaa Glu	cac His	gat Asp	gcc Ala	tct Ser	192
		50				55				60						
gtg Val	gcc Ala	ctg Leu	aca Thr	gcc Ala	act Thr	gcc Ala	gat Asp	tgt Cys	cct Pro	ggg Gly	agg Arg	ggc Gly	ctt Leu	cag Gln	gga Gly	240
65				70				75						80		
acc Thr	gca Ala	cag Gln	gaa Glu	gga Gly	ggg Gly	tgc Cys	agc Ser	tca Ser	gcc Ala	cgt Arg	ttt Phe	caa Gln	atc Ile	cag Gln	cag Gln	288
				85				90						95		
gat Asp	gtt Val	cat His	gac Asp	ctc Leu	cct Pro	gca Ala	gac Asp	act Thr	aat Asn	gga Gly	cag Gln	aac Asn	gtc Val	aca Thr	gca Ala	336
		100						105				110				
gtc Val	tgc Cys	ttc Phe	cct Pro	cac His	ctg Leu	tac Tyr	ggg Gly	ggt Gly	tac Tyr	ccc Pro	aga Arg	tca Ser	ccc Pro	cca Pro	gtc Val	384
		115				120						125				
acc Thr	gac Asp	tgc Cys	atg Met	caa Gln	atc Ile	tct Ser	gtc Val	tca Ser	gag Glu	ttt Phe	ggt Gly	ccc Pro	agc Ser	aca Thr	ttc Phe	432
		130				135				140						
aac Asn	cta Leu	ggg Gly	cat His	gta Val	gga Gly	cca Pro	ccc Pro	tcg Ser	ttt Phe	cac His	gat Asp	aaa Lys	caa Gln	cca Pro	aaa Lys	480
145				150				155						160		
cag Gln	ggc Gly	agt Ser	tac Tyr	gtg Val	atg Met	tgc Cys	gta Val	aga Arg	tgg Trp	cac His	gac Asp	tca Ser	cac His	gtg Val	cgg Pro	528
				165				170						175		
cag Gln	ctg Leu	gaa Glu	ctt Leu	aaa Lys	ctc Leu	cat His	ccg Pro	gac Asp	tcc Ser	aag Lys	gcc Ala	acc Thr	ctg Leu	ttg Leu	tct Ser	576
		180				185						190				
ctc Leu	cac His	aat Asn	caa Gln	tgc Cys	tca Ser	gag Glu	cac His	agc Ser	ctg Leu	caa Gln	ctg Leu	taa *				615

195

200

<210> 234

<211> 204

<212> PRT

<213> Homo sapiens

<400> 234

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Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1          5          10          15
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
 20          25          30
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
 35          40          45
Trp Ala Ser Thr Gln Ile Pro Pro Glu Pro Gln Glu His Asp Ala Ser
 50          55          60
Val Ala Leu Thr Ala Thr Ala Asp Cys Pro Gly Arg Gly Leu Gln Gly
 65          70          75          80
Thr Ala Gln Glu Gly Gly Cys Ser Ser Ala Arg Phe Gln Ile Gln Gln
 85          90          95
Asp Val His Asp Leu Pro Ala Asp Thr Asn Gly Gln Asn Val Thr Ala
 100         105         110
Val Cys Phe Pro His Leu Tyr Gly Gly Tyr Pro Arg Ser Pro Pro Val
 115         120         125
Thr Asp Cys Met Gln Ile Ser Val Ser Glu Phe Gly Pro Ser Thr Phe
 130         135         140
Asn Leu Gly His Val Gly Pro Pro Ser Phe His Asp Lys Gln Pro Lys
 145         150         155         160
Gln Gly Ser Tyr Val Met Cys Val Arg Trp His Asp Ser His Val Pro
 165         170         175
Gln Leu Glu Leu Lys Leu His Pro Asp Ser Lys Ala Thr Leu Leu Ser
 180         185         190
Leu His Asn Gln Cys Ser Glu His Ser Leu Gln Leu
 195         200

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<210> 235

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(597)

<400> 235

atg gct ctc agc ttt tgg ccc ctg ctg ctg ctg ttg ctg ctg ctg atg	48
Met Ala Leu Ser Phe Trp Pro Leu Leu Leu Leu Leu Leu Leu Met	
1 5 10 15	
ctg ctg tcc ttt gca gtg act ctg gcc cct act ggg cct cat tcc ctg	96
Leu Leu Ser Phe Ala Val Thr Leu Ala Pro Thr Gly Pro His Ser Leu	
20 25 30	
gac cct ggt ctc tcc ttc ctg aag tca ttg ctc tcc act ctg gac cag	144
Asp Pro Gly Leu Ser Phe Leu Lys Ser Leu Leu Ser Thr Leu Asp Gln	
35 40 45	
gct ccc cag ggc tcc ctg agc cgc tca cgg ttc ttt aca ttc ctg gcc	192
Ala Pro Gln Gly Ser Leu Ser Arg Ser Arg Phe Phe Thr Phe Leu Ala	
50 55 60	
aac att tct tct tcc ttt gag cct ggg aga atg ggg gaa gga cca gta	240
Asn Ile Ser Ser Ser Phe Glu Pro Gly Arg Met Gly Glu Gly Pro Val	
65 70 75 80	
gga gag ccc cca cct ctc cag ccg cct gct ctg cgg ctc cat gat ttt	288
Gly Glu Pro Pro Pro Leu Gln Pro Pro Ala Leu Arg Leu His Asp Phe	
85 90 95	
cta gtg aca ctg aga ggt agc ccc gac tgg gag cca atg cta ggg ctg	336
Leu Val Thr Leu Arg Gly Ser Pro Asp Trp Glu Pro Met Leu Gly Leu	
100 105 110	
cta ggg gat atg ctg gca ctg ctg gga cag gag cag act ccc cga gat	384
Leu Gly Asp Met Leu Ala Leu Leu Gly Gln Glu Gln Thr Pro Arg Asp	
115 120 125	
ttc ctg gtg cac cag gca ggg gtg ctg ggt gga ctt gtg gag gtg ctg	432
Phe Leu Val His Gln Ala Gly Val Leu Gly Gly Leu Val Glu Val Leu	
130 135 140	
ctg gga gcc tta gtt cct ggg ggc ccc cct acc cca act cag ccc cca	480
Leu Gly Ala Leu Val Pro Gly Gly Pro Pro Thr Pro Thr Gln Pro Pro	
145 150 155 160	

tgc acc cgt gat ggg ccg tct gac tgt gtc ctg gct gct gac tgg ttg 528
 Cys Thr Arg Asp Gly Pro Ser Asp Cys Val Leu Ala Ala Asp Trp Leu
 165 170 175

cct tct ctg ctg ctg ttg tta gag gac caa ttt tcc ctt tgc ccc tca 576
 Pro Ser Leu Leu Leu Leu Leu Glu Asp Gln Phe Ser Leu Cys Pro Ser
 180 185 190

ggg acc ccc ctt ctg ttc taa 597
 Gly Thr Pro Leu Leu Phe *
 195

<210> 236

<211> 198

<212> PRT

<213> Homo sapiens

<400> 236

Met Ala Leu Ser Phe Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu Met
 1 5 10 15
 Leu Leu Ser Phe Ala Val Thr Leu Ala Pro Thr Gly Pro His Ser Leu
 20 25 30
 Asp Pro Gly Leu Ser Phe Leu Lys Ser Leu Leu Ser Thr Leu Asp Gln
 35 40 45
 Ala Pro Gln Gly Ser Leu Ser Arg Ser Arg Phe Phe Thr Phe Leu Ala
 50 55 60
 Asn Ile Ser Ser Ser Phe Glu Pro Gly Arg Met Gly Glu Gly Pro Val
 65 70 75 80
 Gly Glu Pro Pro Pro Leu Gln Pro Pro Ala Leu Arg Leu His Asp Phe
 85 90 95
 Leu Val Thr Leu Arg Gly Ser Pro Asp Trp Glu Pro Met Leu Gly Leu
 100 105 110
 Leu Gly Asp Met Leu Ala Leu Leu Gly Gln Glu Gln Thr Pro Arg Asp
 115 120 125
 Phe Leu Val His Gln Ala Gly Val Leu Gly Gly Leu Val Glu Val Leu
 130 135 140
 Leu Gly Ala Leu Val Pro Gly Gly Pro Pro Thr Pro Thr Gln Pro Pro
 145 150 155 160
 Cys Thr Arg Asp Gly Pro Ser Asp Cys Val Leu Ala Ala Asp Trp Leu
 165 170 175
 Pro Ser Leu Leu Leu Leu Leu Glu Asp Gln Phe Ser Leu Cys Pro Ser
 180 185 190

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<210> 237
<211> 327
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(327)

<400> 237

atg ctg ctg ctg ctg ctg ctg ctg ctg ctg cta ctg ctg cta tta cca 48
Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro
1 5 10 15

cgt gag ccc acc ttt gtg cta atc aag act cgc atc act gcc tta aaa 96
Arg Glu Pro Thr Phe Val Leu Ile Lys Thr Arg Ile Thr Ala Leu Lys
20 25 30

agt ggg cat cct aaa acg tcc aag gaa aac atc agg gga cat gag atg 144
Ser Gly His Pro Lys Thr Ser Lys Glu Asn Ile Arg Gly His Glu Met
 35 40 45

tca gat ggc cct cac aac caa gca ctc tgt ctt gaa gca cta gct aag 192
Ser Asp Gly Pro His Asn Gln Ala Leu Cys Leu Glu Ala Leu Ala Lys
50 55 60

ctg cga atc aag ctg ctt att tgg tta gga gaa cct gtg aaa gac cat 240
Leu Arg Ile Lys Leu Leu Ile Trp Leu Gly Glu Pro Val Lys Asp His
65 70 75 80

agc ttg cat gcc ctg cgg ttc gac tct aga aga tcc ccc cca gca ggc 288
Ser Leu His Ala Leu Arg Phe Asp Ser Arg Arg Ser Pro Pro Ala Gly
85 90 95

cag att gta gta gtt ccc aac ttt ggc tgc aca ttg taa 327
Gln Ile Val Val Val Pro Asn Phe Gly Cys Thr Leu *
100 105

<210> 238

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 238

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Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro
 1          5          10          15
Arg Glu Pro Thr Phe Val Leu Ile Lys Thr Arg Ile Thr Ala Leu Lys
          20          25          30
Ser Gly His Pro Lys Thr Ser Lys Glu Asn Ile Arg Gly His Glu Met
          35          40          45
Ser Asp Gly Pro His Asn Gln Ala Leu Cys Leu Glu Ala Leu Ala Lys
          50          55          60
Leu Arg Ile Lys Leu Leu Ile Trp Leu Gly Glu Pro Val Lys Asp His
65          70          75          80
Ser Leu His Ala Leu Arg Phe Asp Ser Arg Arg Ser Pro Pro Ala Gly
          85          90          95
Gln Ile Val Val Val Pro Asn Phe Gly Cys Thr Leu
          100          105

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<210> 239
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(456)

<400> 239

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atg cct gct tca gac acc agc ccc ctt ctt cgc ctc atc gca ctg agt      48
Met Pro Ala Ser Asp Thr Ser Pro Leu Leu Arg Leu Ile Ala Leu Ser
 1          5          10          15

agt aac atc att gca att gtt ttt cta ata gac tgc tgt gtc tgc cca      96
Ser Asn Ile Ile Ala Ile Val Phe Leu Ile Asp Cys Cys Val Cys Pro
          20          25          30

cta gat ttc aag ctc tct aaa gag gcc cac gat agt gtc act caa atc      144
Leu Asp Phe Lys Leu Ser Lys Glu Ala His Asp Ser Val Thr Gln Ile
          35          40          45

ctc tcc aga cag ccc ttt gga aac ata ttc cat gtt cct ctt ctt agg      192

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<210> 240
<211> 151
<212> PRT
<213> Homo sapiens

<400> 240															
Met	Pro	Ala	Ser	Asp	Thr	Ser	Pro	Leu	Leu	Arg	Leu	Ile	Ala	Leu	Ser
1				5					10					15	
Ser	Asn	Ile	Ile	Ala	Ile	Val	Phe	Leu	Ile	Asp	Cys	Cys	Val	Cys	Pro
			20					25					30		
Leu	Asp	Phe	Lys	Leu	Ser	Lys	Glu	Ala	His	Asp	Ser	Val	Thr	Gln	Ile
			35				40					45			
Leu	Ser	Arg	Gln	Pro	Phe	Gly	Asn	Ile	Phe	His	Val	Pro	Leu	Leu	Arg
			50			55					60				
Asp	Val	Gly	Arg	Ser	Gly	Gly	Gly	Asp	Gly	Ser	Val	Lys	Leu	Glu	Glu

<210>	241	
<211>	579	
<212>	DNA	
<213>	Homo sapiens	
<220>		
<221>	CDS	
<222>	(1)...(579)	
<400>	241	
atg tat agc gcc gat ttt ggc ctg ctt gca ctg cta ccg ctg ccg agc		48
Met Tyr Ser Ala Asp Phe Gly Leu Leu Ala Leu Leu Pro Leu Pro Ser		
1 5 10 15		
caa ggc gcg ccg atg gcc acg acg ccc tta ccg ggc gcc cct acc cca		96
Gln Gly Ala Pro Met Ala Thr Thr Pro Leu Pro Gly Ala Pro Thr Pro		
20 25 30		
tgg gat gtt gcg att aca acc aac tgg acc ggc gct tac cgc aaa gaa		144
Trp Asp Val Ala Ile Thr Thr Asn Trp Thr Gly Ala Tyr Arg Lys Glu		
35 40 45		
tat gcc ctg cac gcg gct tgt acc ggg caa caa aaa aca aaa ata caa		192
Tyr Ala Leu His Ala Ala Cys Thr Gly Gln Gln Lys Thr Lys Ile Gln		
50 55 60		
aaa cgc gtg cgc ata gct ata cat gtt tgc ctg cgt act gca cca ctg		240
Lys Arg Val Arg Ile Ala Ile His Val Cys Leu Arg Thr Ala Pro Leu		
65 70 75 80		
gat aac cta tgt aca gga ttt gct gta aac ccg cct tgg cca cct gcc		288
Asp Asn Leu Cys Thr Gly Phe Ala Val Asn Pro Pro Trp Pro Pro Ala		

	85	90	95	
	gaa ctt acg ctt tcc ctg caa ttc gca gtt ggc tta cac ctt gtg acc			336
	Glu Leu Thr Leu Ser Leu Gln Phe Ala Val Gly Leu His Leu Val Thr			
	100	105	110	
	ggg ggg tta cct ata gta ggg ggg agt gag gga agt ttg cca cac gac			384
	Gly Gly Leu Pro Ile Val Gly Gly Ser Glu Gly Ser Leu Pro His Asp			
	115	120	125	
	cac act ctt aca gca att gct agt aac ccg cct acg cca gcc gcg gaa			432
	His Thr Leu Thr Ala Ile Ala Ser Asn Pro Pro Thr Pro Ala Ala Glu			
	130	135	140	
	cta ccg ctt acc cgc cac ggc gaa cga gaa aga cgc agg cag ctg cct			480
	Leu Pro Leu Thr Arg His Gly Glu Arg Glu Arg Arg Arg Gln Leu Pro			
	145	150	155	160
	gct gtt agt cga ctc tac gag gat ccc cac cct cct cta ggg gca ctc			528
	Ala Val Ser Arg Leu Tyr Glu Asp Pro His Pro Pro Leu Gly Ala Leu			
	165	170	175	
	aat gaa aga acc ggg aag cgc cct gat atg act gtg gtt gga ctg acc			576
	Asn Glu Arg Thr Gly Lys Arg Pro Asp Met Thr Val Val Gly Leu Thr			
	180	185	190	
	tga			579
	*			

<210> 242

<211> 192

<212> PRT

<213> Homo sapiens

<400> 242

Met Tyr Ser Ala Asp Phe Gly Leu Leu Ala Leu Leu Pro Leu Pro Ser	
1 5 10 15	
Gln Gly Ala Pro Met Ala Thr Thr Pro Leu Pro Gly Ala Pro Thr Pro	
20 25 30	
Trp Asp Val Ala Ile Thr Thr Asn Trp Thr Gly Ala Tyr Arg Lys Glu	
35 40 45	


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<210> 243
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(351)
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<400> 243																
atg	gct	cgc	aga	cac	tgc	ttc	tcc	tac	tgg	tta	ctg	gta	tgc	tgg	ttg	48
Met	Ala	Arg	Arg	His	Cys	Phe	Ser	Tyr	Trp	Leu	Leu	Val	Cys	Trp	Leu	
1				5					10					15		
gtg	gta	act	gtg	gca	gaa	gga	caa	gaa	gag	gta	ttt	acg	cct	cct	gga	96
Val	Val	Thr	Val	Ala	Glu	Gly	Gln	Glu	Glu	Val	Phe	Thr	Pro	Pro	Gly	
			20					25					30			
gat	tca	caa	aat	aat	gcg	gac	gct	acc	gac	tgc	cag	atc	ttt	aca	ctc	144
Asp	Ser	Gln	Asn	Asn	Ala	Asp	Ala	Thr	Asp	Cys	Gln	Ile	Phe	Thr	Leu	
		35					40					45				
acc	cct	cca	cct	gcc	ccg	agg	agt	ccg	ttc	tgc	tca	gag	aaa	ggc	cct	192
Thr	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Pro	Phe	Cys	Ser	Glu	Lys	Gly	Pro	

<210> 244
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 244

Met Ala Arg Arg His Cys Phe Ser Tyr Trp Leu Leu Val Cys Trp Leu
 1 5 10 15
 Val Val Thr Val Ala Glu Gly Gln Glu Glu Val Phe Thr Pro Pro Gly
 20 25 30
 Asp Ser Gln Asn Asn Ala Asp Ala Thr Asp Cys Gln Ile Phe Thr Leu
 35 40 45
 Thr Pro Pro Pro Ala Pro Arg Ser Pro Phe Cys Ser Glu Lys Gly Pro
 50 55 60
 Val Leu Leu Leu Gly Leu Glu Glu Ala Lys Ile Leu Cys Asn Asp Cys
 65 70 75 80
 Asn Gly Arg Ser Thr Val Gln Phe His Ile Leu Gly Met Lys Cys Lys
 85 90 95
 Ile Cys Glu Ser Tyr Asn Thr Ala Gln Ala Gly Gly Arg Arg Ile Ser
 100 105 110
 Leu Asp Gln Gln
 115

<210> 245

<211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(327)

<400> 245

atg	ctc	ctg	ctg	ctg	ctc	ctt	gaa	aca	ctg	gct	gtg	ttt	gca	ctg	agg	48
Met	Leu	Leu	Leu	Leu	Leu	Leu	Glu	Thr	Leu	Ala	Val	Phe	Ala	Leu	Arg	
1				5					10					15		

cca	tgc	ctc	agc	cag	cga	ctg	agt	gtg	aca	agg	att	ctc	agt	cct	gtt	96
Pro	Cys	Leu	Ser	Gln	Arg	Leu	Ser	Val	Thr	Arg	Ile	Leu	Ser	Pro	Val	
			20					25					30			

cct	ggg	aga	tgt	gag	att	cct	ttg	ctg	gca	aac	ttc	agc	ttg	aat	att	144
Pro	Gly	Arg	Cys	Glu	Ile	Pro	Leu	Leu	Ala	Asn	Phe	Ser	Leu	Asn	Ile	
		35					40					45				

ccc	cag	gta	caa	tgg	gat	acc	cgt	ggc	tac	act	cta	tca	cat	ctc	ttc	192
Pro	Gln	Val	Gln	Trp	Asp	Thr	Arg	Gly	Tyr	Thr	Leu	Ser	His	Leu	Phe	
	50					55					60					

att	cat	ctt	ctc	agc	aac	tct	cca	ttg	aac	act	tac	act	gtt	cta	gac	240
Ile	His	Leu	Leu	Ser	Asn	Ser	Pro	Leu	Asn	Thr	Tyr	Thr	Val	Leu	Asp	
65					70					75				80		

act	caa	gaa	aga	gca	ctc	ctt	aag	gca	gac	aaa	gtt	gcc	tgc	cct	caa	288
Thr	Gln	Glu	Arg	Ala	Leu	Leu	Lys	Ala	Asp	Lys	Val	Ala	Cys	Pro	Gln	
			85					90					95			

gaa	gct	act	att	cta	gtg	aaa	gaa	gac	aaa	caa	aaa	taa				327
Glu	Ala	Thr	Ile	Leu	Val	Lys	Glu	Asp	Lys	Gln	Lys	*				
			100				105									

<210> 246
 <211> 108
 <212> PRT
 <213> Homo sapiens

Met	Leu	Leu	Leu	Leu	Leu	Leu	Glu	Thr	Leu	Ala	Val	Phe	Ala	Leu	Arg
1				5					10					15	
Pro	Cys	Leu	Ser	Gln	Arg	Leu	Ser	Val	Thr	Arg	Ile	Leu	Ser	Pro	Val
			20					25					30		
Pro	Gly	Arg	Cys	Glu	Ile	Pro	Leu	Leu	Ala	Asn	Phe	Ser	Leu	Asn	Ile
		35					40					45			
Pro	Gln	Val	Gln	Trp	Asp	Thr	Arg	Gly	Tyr	Thr	Leu	Ser	His	Leu	Phe
	50					55					60				
Ile	His	Leu	Leu	Ser	Asn	Ser	Pro	Leu	Asn	Thr	Tyr	Thr	Val	Leu	Asp
65					70					75					80
Thr	Gln	Glu	Arg	Ala	Leu	Leu	Lys	Ala	Asp	Lys	Val	Ala	Cys	Pro	Gln
				85					90					95	
Glu	Ala	Thr	Ile	Leu	Val	Lys	Glu	Asp	Lys	Gln	Lys				
			100					105							

<211> 438

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(438)

<400> 247

atg	agt	ttg	ctg	ttg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ttt	aaa	tgg	48
Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Lys	Trp	
1				5						10					15		
aaa	aga	aga	gta	gta	agt	ggt	cat	ctt	ctc	agc	gtc	tgg	tgc	tgg	tcc	96	
Lys	Arg	Arg	Val	Val	Ser	Gly	His	Leu	Leu	Ser	Val	Trp	Cys	Trp	Ser		
			20					25					30				
cgc	cca	cac	act	gtg	gca	gag	cag	acc	cac	ctg	ttg	tca	ctg	gga	aat	144	
Arg	Pro	His	Thr	Val	Ala	Glu	Gln	Thr	His	Leu	Leu	Ser	Leu	Gly	Asn		
		35					40					45					
gag	ggg	ctg	cag	gta	ctg	ccc	tta	gac	aat	gga	gag	gct	tct	gga	ctg	192	
Glu	Gly	Leu	Gln	Val	Leu	Pro	Leu	Asp	Asn	Gly	Glu	Ala	Ser	Gly	Leu		
	50					55					60						
tca	ctc	caa	ctt	gga	atc	aaa	tgg	acc	act	gag	aaa	ccc	gtg	gaa	gac	240	

<400> 248															
Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Lys	Trp
1				5					10					15	
Lys	Arg	Arg	Val	Val	Ser	Gly	His	Leu	Leu	Ser	Val	Trp	Cys	Trp	Ser
			20					25					30		
Arg	Pro	His	Thr	Val	Ala	Glu	Gln	Thr	His	Leu	Leu	Ser	Leu	Gly	Asn
		35					40					45			
Glu	Gly	Leu	Gln	Val	Leu	Pro	Leu	Asp	Asn	Gly	Glu	Ala	Ser	Gly	Leu
	50					55					60				
Ser	Leu	Gln	Leu	Gly	Ile	Lys	Trp	Thr	Thr	Glu	Lys	Pro	Val	Glu	Asp
65					70					75				80	
Ser	Arg	Ser	Lys	Glu	Ile	Thr	Lys	Ile	Arg	Asn	Ala	Ser	Met	Cys	Thr
				85					90					95	
Gln	Leu	Pro	Pro	Ser	Val	Gly	Gly	Gly	Thr	Cys	Asn	Ser	Leu	Trp	Tyr

100 105 110
 Thr Arg Val Val Gln Glu Ile Val Leu His Glu Arg Ser Glu Glu Lys
 115 120 125
 Trp Arg Asp Ser Arg Ser Gly Lys Phe Thr Phe Gln Asp Val Arg Lys
 130 135 140
 Arg
 145

<210> 249
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(552)

<400> 249
 atg aaa gtg gtg gtg gtg atg gtg gta ata ctg gtg gtg gtg aca ttg 48
 Met Lys Val Val Val Val Met Val Val Ile Leu Val Val Val Thr Leu
 1 5 10 15
 gtg gtg gtg gtg atg gtg gtg ata ctg gtg atg gtg gtg atg gtg gtg 96
 Val Val Val Val Met Val Val Ile Leu Val Met Val Val Met Val Val
 20 25 30
 gcg ctg gtg acc ctg aca tgg ggt cca gta gca gtg aca gtg gat gca 144
 Ala Leu Val Thr Leu Thr Trp Gly Pro Val Ala Val Thr Val Asp Ala
 35 40 45
 ggc tcc tgt ctc tca gca aac ctg ctg ggc gac agc gga ctc aga tgc 192
 Gly Ser Cys Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys
 50 55 60
 ctt ctg gaa tgt ctg ccg cag gtg ccc atc tcc ggt ttg ctt gac ctg 240
 Leu Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu
 65 70 75 80
 ggc tct gag cag agc ttc cgg att cac ttc tcc aga gag gac cag gct 288
 Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln Ala
 85 90 95
 ggg aag aca ctc agg cta agt gag tgc agc ttc cgg cca gag cac gtg 336

Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His Val
 100 105 110

tcc agg ctg gcc acc ggc ttg agc aag tcc ctg cag ctg acg gag ctc 384
 Ser Arg Leu Ala Thr Gly Leu Ser Lys Ser Leu Gln Leu Thr Glu Leu
 115 120 125

acg ctg acc cag tgc tgc ctg ggc cag aag cag ctg gcc atc ctc ctg 432
 Thr Leu Thr Gln Cys Cys Leu Gly Gln Lys Gln Leu Ala Ile Leu Leu
 130 135 140

agc ttg gtg ggg cga ccc gca ggg ctg ttc agc ctc aga gac aac tgc 480
 Ser Leu Val Gly Arg Pro Ala Gly Leu Phe Ser Leu Arg Asp Asn Cys
 145 150 155 160

aga gct aca aag aca gca cat cca caa atg gag acc atc aca tca tcg 528
 Arg Ala Thr Lys Thr Ala His Pro Gln Met Glu Thr Ile Thr Ser Ser
 165 170 175

aca ata gca gct tct gtt tac taa 552
 Thr Ile Ala Ala Ser Val Tyr *
 180

<210> 250

<211> 183

<212> PRT

<213> Homo sapiens

<400> 250

Met Lys Val Val Val Val Met Val Val Ile Leu Val Val Val Thr Leu
 1 5 10 15

Val Val Val Val Met Val Val Ile Leu Val Met Val Val Met Val Val
 20 25 30

Ala Leu Val Thr Leu Thr Trp Gly Pro Val Ala Val Thr Val Asp Ala
 35 40 45

Gly Ser Cys Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys
 50 55 60

Leu Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu
 65 70 75 80

Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln Ala
 85 90 95

Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His Val

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<210> 251
<211> 546
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(546)

atg aaa aca ttg gat cgg aag gtt ttc ttc ctg tct tca ctg ctc att 48
Met Lys Thr Leu Asp Arg Lys Val Phe Phe Leu Ser Ser Leu Leu Ile
1 5 10 15

gga ctt tca gga ctg gaa gag ccc ctc tac ctt aaa ttt aga gtt aca 96
Gly Leu Ser Gly Leu Glu Glu Pro Leu Tyr Leu Lys Phe Arg Val Thr
20 25 30

ggt tca ttg gaa aga gca tca acc caa cct gct tac atc aga gac ctg 144
Gly Ser Leu Glu Arg Ala Ser Thr Gln Pro Ala Tyr Ile Arg Asp Leu
35 40 45

aac act cag tgt gac tgt gcg aac tcc ccg tac agg aca ttt att aat 192
Asn Thr Gln Cys Asp Cys Ala Asn Ser Pro Tyr Arg Thr Phe Ile Asn
50 55 60

gct agt atg cac ttt ctc cct ctt agt aat aac att cca gag tcc tct 240
Ala Ser Met His Phe Leu Pro Leu Ser Asn Asn Ile Pro Glu Ser Ser
65 70 75 80

tgg gga gaa atc tcc att gac ttt gtg gaa ctg caa ggc aag gtg cct 288

Trp Gly Glu Ile Ser Ile Asp Phe Val Glu Leu Gln Gly Lys Val Pro
 85 90 95
 agt tct cca atc acc aag atg tgc aca cat gac cca ttg gcc aag tgg 336
 Ser Ser Pro Ile Thr Lys Met Cys Thr His Asp Pro Leu Ala Lys Trp
 100 105 110
 aca ctc tct ccc aaa tct tcg aat ctc aag cag atg gat gca agg atg 384
 Thr Leu Ser Pro Lys Ser Ser Asn Leu Lys Gln Met Asp Ala Arg Met
 115 120 125
 gaa aac agc tgg aat cga ctc att tca gtg gga tca gaa agg gca gcc 432
 Glu Asn Ser Trp Asn Arg Leu Ile Ser Val Gly Ser Glu Arg Ala Ala
 130 135 140
 aca gag tta ggt gag aag gca cag ctg aag cga tgg aag att tac atc 480
 Thr Glu Leu Gly Glu Lys Ala Gln Leu Lys Arg Trp Lys Ile Tyr Ile
 145 150 155 160
 ata tct gtc agc atg tca ata acc cat cct gaa att cag gaa agg ctg 528
 Ile Ser Val Ser Met Ser Ile Thr His Pro Glu Ile Gln Glu Arg Leu
 165 170 175
 aaa aac tgt cta act tga 546
 Lys Asn Cys Leu Thr *
 180

<210> 252
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 252
 Met Lys Thr Leu Asp Arg Lys Val Phe Phe Leu Ser Ser Leu Leu Ile
 1 5 10 15
 Gly Leu Ser Gly Leu Glu Glu Pro Leu Tyr Leu Lys Phe Arg Val Thr
 20 25 30
 Gly Ser Leu Glu Arg Ala Ser Thr Gln Pro Ala Tyr Ile Arg Asp Leu
 35 40 45
 Asn Thr Gln Cys Asp Cys Ala Asn Ser Pro Tyr Arg Thr Phe Ile Asn
 50 55 60
 Ala Ser Met His Phe Leu Pro Leu Ser Asn Asn Ile Pro Glu Ser Ser

65 70 75 80
 Trp Gly Glu Ile Ser Ile Asp Phe Val Glu Leu Gln Gly Lys Val Pro
 85 90 95
 Ser Ser Pro Ile Thr Lys Met Cys Thr His Asp Pro Leu Ala Lys Trp
 100 105 110
 Thr Leu Ser Pro Lys Ser Ser Asn Leu Lys Gln Met Asp Ala Arg Met
 115 120 125
 Glu Asn Ser Trp Asn Arg Leu Ile Ser Val Gly Ser Glu Arg Ala Ala
 130 135 140
 Thr Glu Leu Gly Glu Lys Ala Gln Leu Lys Arg Trp Lys Ile Tyr Ile
 145 150 155 160
 Ile Ser Val Ser Met Ser Ile Thr His Pro Glu Ile Gln Glu Arg Leu
 165 170 175
 Lys Asn Cys Leu Thr
 180

<210> 253
 <211> 426
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(426)

<400> 253

atg agg ccc cgg aaa gcc ttc ctg ctc ctg ctg ctc ttg ggg ctg gtg 48
 Met Arg Pro Arg Lys Ala Phe Leu Leu Leu Leu Leu Leu Gly Leu Val
 1 5 10 15

cag ctg ctg gcc gtg gcg ggt gcc gag ggc ccg gac gag ggg ctc cca 96
 Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Gly Leu Pro
 20 25 30

ctg tct tct ggc att tgc ttc cta aac tac aac cca gcc agc tcc act 144
 Leu Ser Ser Gly Ile Cys Phe Leu Asn Tyr Asn Pro Ala Ser Ser Thr
 35 40 45

gct tac ttc ttg gac att gtt gtc cag ccc ctt gga aaa cag ttg gaa 192
 Ala Tyr Phe Leu Asp Ile Val Val Gln Pro Leu Gly Lys Gln Leu Glu
 50 55 60

cag ccg ttg ggc tct gag caa caa ggc cct ttt att tca gtt aga tgc 240

Gln Pro Leu Gly Ser Glu Gln Gln Gly Pro Phe Ile Ser Val Arg Cys
65 70 75 80

tgg gct cgg gac ctg cag ccc gcc atg cct gag ctt ccc acc cac tcc 288
Trp Ala Arg Asp Leu Gln Pro Ala Met Pro Glu Leu Pro Thr His Ser
85 90 95

atg ggc tcc tgt gcg gcc cga gcc tcc ccg acg agc gcc acc ccc tgc 336
Met Gly Ser Cys Ala Ala Arg Ala Ser Pro Thr Ser Ala Thr Pro Cys
100 105 110

tcc acg gcg ccc agt ccc atc gac cac cca agg gct gag gag tgc gag 384
Ser Thr Ala Pro Ser Pro Ile Asp His Pro Arg Ala Glu Glu Cys Glu
115 120 125

cgc acg gcg cgg gac tgg cag cct gca gat ggc cta ctg tga 426
Arg Thr Ala Arg Asp Trp Gln Pro Ala Asp Gly Leu Leu *
130 135 140

<210> 254

<211> 141

<212> PRT

<213> Homo sapiens

<400> 254

Met Arg Pro Arg Lys Ala Phe Leu Leu Leu Leu Leu Gly Leu Val
1 5 10 15
Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Gly Leu Pro
20 25 30
Leu Ser Ser Gly Ile Cys Phe Leu Asn Tyr Asn Pro Ala Ser Ser Thr
35 40 45
Ala Tyr Phe Leu Asp Ile Val Val Gln Pro Leu Gly Lys Gln Leu Glu
50 55 60
Gln Pro Leu Gly Ser Glu Gln Gln Gly Pro Phe Ile Ser Val Arg Cys
65 70 75 80
Trp Ala Arg Asp Leu Gln Pro Ala Met Pro Glu Leu Pro Thr His Ser
85 90 95
Met Gly Ser Cys Ala Ala Arg Ala Ser Pro Thr Ser Ala Thr Pro Cys
100 105 110
Ser Thr Ala Pro Ser Pro Ile Asp His Pro Arg Ala Glu Glu Cys Glu
115 120 125
Arg Thr Ala Arg Asp Trp Gln Pro Ala Asp Gly Leu Leu

130

135

140

<210> 255

<211> 942

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(942)

<400> 255

atg gag gat tat ata cat aag ctc gtt tat aca gtg ttt gct tgt ggg	48
Met Glu Asp Tyr Ile His Lys Leu Val Tyr Thr Val Phe Ala Cys Gly	
1 5 10 15	
agg cac cct gct ctc ctc ctt ctc ttt gtc cct gtg ctg ccg agt gcc	96
Arg His Pro Ala Leu Leu Leu Leu Phe Val Pro Val Leu Pro Ser Ala	
20 25 30	
ggt tcg tcg ccg ctg cct ggc cat gtc tta agc atc ttt tct cct ccc	144
Gly Ser Ser Pro Leu Pro Gly His Val Leu Ser Ile Phe Ser Pro Pro	
35 40 45	
gcg cgc ata ccg cat gcc cgt tcg gtg tcc tcc cag ctc ttc ccg tat	192
Ala Arg Ile Pro His Ala Arg Ser Val Ser Ser Gln Leu Phe Pro Tyr	
50 55 60	
gca gcc gtt gcc agc ttc gga ccc tcc ctg cgg gta gtg gag ttt tta	240
Ala Ala Val Ala Ser Phe Gly Pro Ser Leu Arg Val Val Glu Phe Leu	
65 70 75 80	
gag aga ctc ctt ctc gtc cgt gct gct gat cgg agc tgt cgc agc cgt	288
Glu Arg Leu Leu Leu Val Arg Ala Ala Asp Arg Ser Cys Arg Ser Arg	
85 90 95	
ttc gct cct att cgc gac cga ggt ctc cgc agc tcg cgc tgt cgc aca	336
Phe Ala Pro Ile Arg Asp Arg Gly Leu Arg Ser Ser Arg Cys Arg Thr	
100 105 110	
gat ctc cgt gtc agc ggc tgg cat ggc ctc cct ctc gat ttg cct aaa	384
Asp Leu Arg Val Ser Gly Trp His Gly Leu Pro Leu Asp Leu Pro Lys	
115 120 125	

gag tat aca tat gct tgc tat ata aac tgc act gcc tct gcc gga att	432
Glu Tyr Thr Tyr Ala Cys Tyr Ile Asn Cys Thr Ala Ser Ala Gly Ile	
130 135 140	
gtc acc gag atg ctc agg cct ttc atc act ctt gtg tct aga gcc gcc	480
Val Thr Glu Met Leu Arg Pro Phe Ile Thr Leu Val Ser Arg Ala Ala	
145 150 155 160	
agg tgg tcc cag gac ccc ttt tca cct agc agt tcc gca gcc cat cgg	528
Arg Trp Ser Gln Asp Pro Phe Ser Pro Ser Ser Ser Ala Ala His Arg	
165 170 175	
caa tcc aca ccc cag atc cat ccc tgt atc gtg agc caa cct tcc tgc	576
Gln Ser Thr Pro Gln Ile His Pro Cys Ile Val Ser Gln Pro Ser Cys	
180 185 190	
aaa gtc ctc gtg ggc atc ggc atg tcc tat ttc tct ttc ctt ggg gca	624
Lys Val Leu Val Gly Ile Gly Met Ser Tyr Phe Ser Phe Leu Gly Ala	
195 200 205	
tcc tcg tca tta atg acc cca tcc gcg aca atc cta ccg ctg ctg tcc	672
Ser Ser Ser Leu Met Thr Pro Ser Ala Thr Ile Leu Pro Leu Leu Ser	
210 215 220	
tgc cgt gcg tct ctg acg gtg agc tta gtc agt cgt ctt cgc agt aga	720
Cys Arg Ala Ser Leu Thr Val Ser Leu Val Ser Arg Leu Arg Ser Arg	
225 230 235 240	
cac agc tcc cgg ata gct gct acc aag ttc gac gca tct ata tat cgc	768
His Ser Ser Arg Ile Ala Ala Thr Lys Phe Asp Ala Ser Ile Tyr Arg	
245 250 255	
tgc gcg tca gac gcc ggc gac aca cgc atc ttc cgt agt cat gcc ggg	816
Cys Ala Ser Asp Ala Gly Asp Thr Arg Ile Phe Arg Ser His Ala Gly	
260 265 270	
aga cgt cag ccg agc agt aca tat cgc gtt gta ccg aca atc cta agt	864
Arg Arg Gln Pro Ser Ser Thr Tyr Arg Val Val Pro Thr Ile Leu Ser	
275 280 285	
gca atc gat gtg gtt gtc gca agc tcc gtc aca agc tgc cgc gtc ttc	912
Ala Ile Asp Val Val Val Ala Ser Ser Val Thr Ser Cys Arg Val Phe	

290

295

300

gtg gct aac agc ggc gca tgt gcg ccc tga
 Val Ala Asn Ser Gly Ala Cys Ala Pro *
 305 310

942

<210> 256

<211> 313

<212> PRT

<213> Homo sapiens

<400> 256

Met Glu Asp Tyr Ile His Lys Leu Val Tyr Thr Val Phe Ala Cys Gly
 1 5 10 15
 Arg His Pro Ala Leu Leu Leu Leu Phe Val Pro Val Leu Pro Ser Ala
 20 25 30
 Gly Ser Ser Pro Leu Pro Gly His Val Leu Ser Ile Phe Ser Pro Pro
 35 40 45
 Ala Arg Ile Pro His Ala Arg Ser Val Ser Ser Gln Leu Phe Pro Tyr
 50 55 60
 Ala Ala Val Ala Ser Phe Gly Pro Ser Leu Arg Val Val Glu Phe Leu
 65 70 75 80
 Glu Arg Leu Leu Leu Val Arg Ala Ala Asp Arg Ser Cys Arg Ser Arg
 85 90 95
 Phe Ala Pro Ile Arg Asp Arg Gly Leu Arg Ser Ser Arg Cys Arg Thr
 100 105 110
 Asp Leu Arg Val Ser Gly Trp His Gly Leu Pro Leu Asp Leu Pro Lys
 115 120 125
 Glu Tyr Thr Tyr Ala Cys Tyr Ile Asn Cys Thr Ala Ser Ala Gly Ile
 130 135 140
 Val Thr Glu Met Leu Arg Pro Phe Ile Thr Leu Val Ser Arg Ala Ala
 145 150 155 160
 Arg Trp Ser Gln Asp Pro Phe Ser Pro Ser Ser Ser Ala Ala His Arg
 165 170 175
 Gln Ser Thr Pro Gln Ile His Pro Cys Ile Val Ser Gln Pro Ser Cys
 180 185 190
 Lys Val Leu Val Gly Ile Gly Met Ser Tyr Phe Ser Phe Leu Gly Ala
 195 200 205
 Ser Ser Ser Leu Met Thr Pro Ser Ala Thr Ile Leu Pro Leu Leu Ser
 210 215 220
 Cys Arg Ala Ser Leu Thr Val Ser Leu Val Ser Arg Leu Arg Ser Arg
 225 230 235 240

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<210> 257
<211> 291
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(291)

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<400> 257																
atg	ctt	tgg	ctc	ctt	ttg	gct	ctt	ttt	gcc	ccg	ggt	cgg	gcg	ggg	ggc	48
Met	Leu	Trp	Leu	Leu	Leu	Ala	Leu	Phe	Ala	Pro	Gly	Arg	Ala	Gly	Gly	
1		5			10				15							
ggg	ggg	tgg	ggg	tgc	atc	ttc	cct	gat	aca	cca	cac	tct	cca	ttc	cct	96
Gly	Gly	Trp	Gly	Cys	Ile	Phe	Pro	Asp	Thr	Pro	His	Ser	Pro	Phe	Pro	
			20		25				30							
ggg	ata	tat	gac	act	gat	tgg	gct	acc	acg	atc	ggg	gac	tcc	aca	cca	144
Gly	Ile	Tyr	Asp	Thr	Asp	Trp	Ala	Thr	Thr	Ile	Gly	Asp	Ser	Thr	Pro	
35			40				45									
cta	cta	tgg	ccc	ttc	att	tct	gtg	gct	ctg	tgc	tcc	tcc	agt	gca	ctt	192
Leu	Leu	Trp	Pro	Phe	Ile	Ser	Val	Ala	Leu	Cys	Ser	Ser	Ser	Ala	Leu	
50		55				60										
cct	gca	ggg	cac	ccg	gca	ttc	ccc	aat	cct	aga	cgc	tac	gca	gat	gcc	240
Pro	Ala	Gly	His	Pro	Ala	Phe	Pro	Asn	Pro	Arg	Arg	Tyr	Ala	Asp	Ala	
65		70				75					80					
agc	cat	gca	gaa	tca	cat	acc	atc	tta	cct	gct	gag	ctc	tcc	cct	ttg	288
Ser	His	Ala	Glu	Ser	His	Thr	Ile	Leu	Pro	Ala	Glu	Leu	Ser	Pro	Leu	

260

85

90

95

tga
*

291

<210> 258

<211> 96

<212> PRT

<213> Homo sapiens

<400> 258

Met Leu Trp Leu Leu Leu Ala Leu Phe Ala Pro Gly Arg Ala Gly Gly
1 5 10 15
Gly Gly Trp Gly Cys Ile Phe Pro Asp Thr Pro His Ser Pro Phe Pro
20 25 30
Gly Ile Tyr Asp Thr Asp Trp Ala Thr Thr Ile Gly Asp Ser Thr Pro
35 40 45
Leu Leu Trp Pro Phe Ile Ser Val Ala Leu Cys Ser Ser Ser Ala Leu
50 55 60
Pro Ala Gly His Pro Ala Phe Pro Asn Pro Arg Arg Tyr Ala Asp Ala
65 70 75 80
Ser His Ala Glu Ser His Thr Ile Leu Pro Ala Glu Leu Ser Pro Leu
85 90 95

<210> 259

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(231)

<400> 259

atg aaa ctc atg gaa aca ctt aac cag tgc ata aac gct ggt cat gaa
Met Lys Leu Met Glu Thr Leu Asn Gln Cys Ile Asn Ala Gly His Glu
1 5 10 15

48

atg acg aag gct atc gcc att gca cag ttt aat gat gac agc ccg gaa
Met Thr Lys Ala Ile Ala Ile Ala Gln Phe Asn Asp Asp Ser Pro Glu
20 25 30

96

gcg agg aaa ata acc cgg cgc tgg aga ata ggt gaa gca gcg gat tta 144
 Ala Arg Lys Ile Thr Arg Arg Trp Arg Ile Gly Glu Ala Ala Asp Leu
 35 40 45

gtt ggg gtt tct tct cag gct atc aga gat gcc gag aaa gca ggg cga 192
 Val Gly Val Ser Ser Gln Ala Ile Arg Asp Ala Glu Lys Ala Gly Arg
 50 55 60

cta ccg cac ccg gat atg gaa att cga gga cgg tgt tga 231
 Leu Pro His Pro Asp Met Glu Ile Arg Gly Arg Cys *
 65 70 75

<210> 260

<211> 76

<212> PRT

<213> Homo sapiens

<400> 260

Met Lys Leu Met Glu Thr Leu Asn Gln Cys Ile Asn Ala Gly His Glu
 1 5 10 15
 Met Thr Lys Ala Ile Ala Ile Ala Gln Phe Asn Asp Asp Ser Pro Glu
 20 25 30
 Ala Arg Lys Ile Thr Arg Arg Trp Arg Ile Gly Glu Ala Ala Asp Leu
 35 40 45
 Val Gly Val Ser Ser Gln Ala Ile Arg Asp Ala Glu Lys Ala Gly Arg
 50 55 60
 Leu Pro His Pro Asp Met Glu Ile Arg Gly Arg Cys
 65 70 75

<210> 261

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(375)

<400> 261

atg aag ttc ctg ctc ctg gtc ttg gca gcc ctc gga ttc ctg acc cag 48
 Met Lys Phe Leu Leu Leu Val Leu Ala Ala Leu Gly Phe Leu Thr Gln

262

1	5	10	15	
gtg atc cca ggt gcg gat tct gcc gta aaa tgc gcc cct ggc gac tca				96
Val Ile Pro Gly Ala Asp Ser Ala Val Lys Cys Ala Pro Gly Asp Ser				
	20	25	30	
cga cca gga cgc att ccg cac cgc tcc ccc acg ccc cgc agc ccg ccc				144
Arg Pro Gly Arg Ile Pro His Arg Ser Pro Thr Pro Arg Ser Pro Pro				
	35	40	45	
tcg agg ctg att gat ttg tgc cag tct cta ccg cca tct gcc ggc agc				192
Ser Arg Leu Ile Asp Leu Cys Gln Ser Leu Pro Pro Ser Ala Gly Ser				
	50	55	60	
act cgg tac acc cgc gcc ctg gag gtc gca cgc gct ggc caa acg ggc				240
Thr Arg Tyr Thr Arg Ala Leu Glu Val Ala Arg Ala Gly Gln Thr Gly				
	65	70	75	80
gca cca gac act ttt cag ggc cct gcc aaa gac ctc cca atg tct act				288
Ala Pro Asp Thr Phe Gln Gly Pro Ala Lys Asp Leu Pro Met Ser Thr				
	85	90	95	
ggc gtc cca gac aca aga gat cca ggc caa gac tca cac ttc aca aga				336
Gly Val Pro Asp Thr Arg Asp Pro Gly Gln Asp Ser His Phe Thr Arg				
	100	105	110	
tac aca gac acg ggc ctt agg gaa cag gaa att cca tga				375
Tyr Thr Asp Thr Gly Leu Arg Glu Gln Glu Ile Pro *				
	115	120		

<210> 262

<211> 124

<212> PRT

<213> Homo sapiens

<400> 262

Met Lys Phe Leu Leu Leu Val Leu Ala Ala Leu Gly Phe Leu Thr Gln	
1 5 10 15	
Val Ile Pro Gly Ala Asp Ser Ala Val Lys Cys Ala Pro Gly Asp Ser	
20 25 30	
Arg Pro Gly Arg Ile Pro His Arg Ser Pro Thr Pro Arg Ser Pro Pro	
35 40 45	

```
<210> 263
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(420)
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<400> 263																
atg	aaa	gag	gca	ttg	acc	aac	cag	aca	cca	atg	act	caa	caa	ctt	gat	48
Met	Lys	Glu	Ala	Leu	Thr	Asn	Gln	Thr	Pro	Met	Thr	Gln	Gln	Leu	Asp	
				5					10					15		
att	agc	ctg	att	tta	ctg	atg	gcc	act	tgg	gaa	ctg	gtg	caa	gga	gtg	96
Ile	Ser	Leu	Ile	Leu	Leu	Met	Ala	Thr	Trp	Glu	Leu	Val	Gln	Gly	Val	
				20					25					30		
cag	agg	att	cga	gta	tca	ctt	att	gtt	ctt	cct	gat	gac	cca	ctg	gag	144
Gln	Arg	Ile	Arg	Val	Ser	Leu	Ile	Val	Leu	Pro	Asp	Asp	Pro	Leu	Glu	
				35					40					45		
gac	ttg	cgc	ttc	tat	tct	tac	aca	ttt	gtg	tcc	ttt	gga	ggt	aga	gtt	192
Asp	Leu	Arg	Phe	Tyr	Ser	Tyr	Thr	Phe	Val	Ser	Phe	Gly	Val	Arg	Val	
				50					55					60		
cat	ggc	tct	act	ctt	gcc	ata	cga	cac	att	aaa	ata	caa	gct	atg	gct	240
His	Gly	Ser	Thr	Leu	Ala	Ile	Arg	His	Ile	Lys	Ile	Gln	Ala	Met	Ala	
				65					70					75	80	
gct	gct	ggc	cac	ttt	gaa	ttc	cat	ctt	ggc	aga	gaa	gtc	cgt	gaa	ggc	288
Ala	Ala	Gly	His	Phe	Glu	Phe	His	Leu	Gly	Arg	Glu	Val	Arg	Glu	Gly	

264

85

90

95

cac tta gaa gtt att ttc caa aca tgc aat gga aag tgt atc tct gtg 336
His Leu Glu Val Ile Phe Gln Thr Cys Asn Gly Lys Cys Ile Ser Val
100 105 110

act aaa caa gtg gac tgt ggt ggc cat agt aga gca cga ctc aga ttg 384
Thr Lys Gln Val Asp Cys Gly Gly His Ser Arg Ala Arg Leu Arg Leu
115 120 125

tcc tct gaa aaa acc tgc tgt aga aag cat att tga 420
Ser Ser Glu Lys Thr Cys Cys Arg Lys His Ile *
130 135

<210> 264

<211> 139

<212> PRT

<213> Homo sapiens

<400> 264

Met Lys Glu Ala Leu Thr Asn Gln Thr Pro Met Thr Gln Gln Leu Asp
1 5 10 15
Ile Ser Leu Ile Leu Leu Met Ala Thr Trp Glu Leu Val Gln Gly Val
20 25 30
Gln Arg Ile Arg Val Ser Leu Ile Val Leu Pro Asp Asp Pro Leu Glu
35 40 45
Asp Leu Arg Phe Tyr Ser Tyr Thr Phe Val Ser Phe Gly Val Arg Val
50 55 60
His Gly Ser Thr Leu Ala Ile Arg His Ile Lys Ile Gln Ala Met Ala
65 70 75 80
Ala Ala Gly His Phe Glu Phe His Leu Gly Arg Glu Val Arg Glu Gly
85 90 95
His Leu Glu Val Ile Phe Gln Thr Cys Asn Gly Lys Cys Ile Ser Val
100 105 110
Thr Lys Gln Val Asp Cys Gly Gly His Ser Arg Ala Arg Leu Arg Leu
115 120 125
Ser Ser Glu Lys Thr Cys Cys Arg Lys His Ile
130 135

<210> 265

<211> 477

<212> DNA

103330 226660

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(477)

<400> 265

atg ttt tat tgg ttg gtg caa cgg gta gcc tgt gtt tta ctg tta act	48
Met Phe Tyr Trp Leu Val Gln Arg Val Ala Cys Val Leu Leu Leu Thr	
1 5 10 15	
gca atg ctt ttt caa acg gat gct ttt gaa aca ccc tgg aat ata gtt	96
Ala Met Leu Phe Gln Thr Asp Ala Phe Glu Thr Pro Trp Asn Ile Val	
20 25 30	
ggc aga atg aat aaa gga atg aat aaa agc att gtt cac ata atg cga	144
Gly Arg Met Asn Lys Gly Met Asn Lys Ser Ile Val His Ile Met Arg	
35 40 45	
tat aac ttt cta gaa ggt caa att aac cct act ttc gat gta gaa atg	192
Tyr Asn Phe Leu Glu Gly Gln Ile Asn Pro Thr Phe Asp Val Glu Met	
50 55 60	
act aac ata acc gaa gat cta atg gtg atg tgg tca tgc aca cag tgt	240
Thr Asn Ile Thr Glu Asp Leu Met Val Met Trp Ser Cys Thr Gln Cys	
65 70 75 80	
gta ggt gct acc aac tgt tgc aga cac agt tca tct cag aac aga aag	288
Val Gly Ala Thr Asn Cys Cys Arg His Ser Ser Ser Gln Asn Arg Lys	
85 90 95	
cat gaa act cta gcc aca gga atc aga atc ctt ctt ccc caa ggg tca	336
His Glu Thr Leu Ala Thr Gly Ile Arg Ile Leu Leu Pro Gln Gly Ser	
100 105 110	
atc act cat tcc cca gct gct gaa agt gtg gct gcc aat tgt tta cag	384
Ile Thr His Ser Pro Ala Ala Glu Ser Val Ala Ala Asn Cys Leu Gln	
115 120 125	
ctg tat cct tct ctc aag cat tac tct cag tct ctg gga gcc aag tct	432
Leu Tyr Pro Ser Leu Lys His Tyr Ser Gln Ser Leu Gly Ala Lys Ser	
130 135 140	

tct gga aat gtc tgg gag gct ata cta gga agg aga ggg tgg tag
 Ser Gly Asn Val Trp Glu Ala Ile Leu Gly Arg Arg Gly Trp *
 145 150 155

477

<210> 266
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 266

Met Phe Tyr Trp Leu Val Gln Arg Val Ala Cys Val Leu Leu Leu Thr
 1 5 10 15
 Ala Met Leu Phe Gln Thr Asp Ala Phe Glu Thr Pro Trp Asn Ile Val
 20 25 30
 Gly Arg Met Asn Lys Gly Met Asn Lys Ser Ile Val His Ile Met Arg
 35 40 45
 Tyr Asn Phe Leu Glu Gly Gln Ile Asn Pro Thr Phe Asp Val Glu Met
 50 55 60
 Thr Asn Ile Thr Glu Asp Leu Met Val Met Trp Ser Cys Thr Gln Cys
 65 70 75 80
 Val Gly Ala Thr Asn Cys Cys Arg His Ser Ser Ser Gln Asn Arg Lys
 85 90 95
 His Glu Thr Leu Ala Thr Gly Ile Arg Ile Leu Leu Pro Gln Gly Ser
 100 105 110
 Ile Thr His Ser Pro Ala Ala Glu Ser Val Ala Ala Asn Cys Leu Gln
 115 120 125
 Leu Tyr Pro Ser Leu Lys His Tyr Ser Gln Ser Leu Gly Ala Lys Ser
 130 135 140
 Ser Gly Asn Val Trp Glu Ala Ile Leu Gly Arg Arg Gly Trp
 145 150 155

<210> 267
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(603)

<400> 267

atg gct gca gct tgg acc gtg gtg ctg gtg act ttg gtg cta ggc ttg

48

Met	Ala	Ala	Ala	Trp	Thr	Val	Val	Leu	Val	Thr	Leu	Val	Leu	Gly	Leu		
1				5				10						15			
gcc	gtg	gca	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag		96
Ala	Val	Ala	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys		
			20					25						30			
ggc	tgc	cac	att	ggc	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg		144
Gly	Cys	His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala		
		35					40						45				
agc	ttc	aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa		192
Ser	Phe	Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys		
	50					55					60						
aac	tgg	agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg		240
Asn	Trp	Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg		
65					70					75					80		
ctt	ctc	cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc		288
Leu	Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala		
				85					90					95			
ctg	acg	ctg	aag	gtc	ctg	gag	gcc	gct	gct	ggc	cca	gcc	ctg	gag	gac		336
Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp		
			100				105						110				
gtc	cta	gac	cag	ccc	ctt	cac	acc	ctg	cac	cac	atc	ctc	tcc	cag	ctc		384
Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu		
		115				120						125					
cag	gcc	tgt	atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc		432
Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly		
	130					135					140						
cgc	ctc	cac	cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag		480
Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu		
145					150					155					160		
tcc	gct	ggc	tgc	ctg	gag	gca	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	ctc		528
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu		
				165				170						175			

ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga 576
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190

acg tca acc cac cct gag tcc acc tga 603
 Thr Ser Thr His Pro Glu Ser Thr *
 195 200

<210> 268
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 268
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
 20 25 30
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 35 40 45
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
 50 55 60
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65 70 75 80
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
 100 105 110
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 130 135 140
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 145 150 155 160
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 165 170 175
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190
 Thr Ser Thr His Pro Glu Ser Thr
 195 200

<210> 269

<211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(624)

<400> 269

atg gga aga atc ccg gta att ctg ctg ctg gct gcc ccc cct gtc tcc	48
Met Gly Arg Ile Pro Val Ile Leu Leu Leu Ala Ala Pro Pro Val Ser	
1 5 10 15	
ctg tca gcg gtg cga cta gct act agt agt agg agg act aag cca cta	96
Leu Ser Ala Val Arg Leu Ala Thr Ser Ser Arg Arg Thr Lys Pro Leu	
20 25 30	
acg agc ttc ctc gct ctg cag aaa cgt ttg ggc ctc gtc cca tcg gcg	144
Thr Ser Phe Leu Ala Leu Gln Lys Arg Leu Gly Leu Val Pro Ser Ala	
35 40 45	
gac tat atg cag tat ctc cct att gta cgt cgg ggc agg cag cat agc	192
Asp Tyr Met Gln Tyr Leu Pro Ile Val Arg Arg Gly Arg Gln His Ser	
50 55 60	
att gtg gcg tcc acc cag acg ggc cgg gct tcg gta gtg act gct act	240
Ile Val Ala Ser Thr Gln Thr Gly Arg Ala Ser Val Val Thr Ala Thr	
65 70 75 80	
tac tct ggc gcg cgc gat atc tca ggc atc agt ttt cga acc agg gct	288
Tyr Ser Gly Ala Arg Asp Ile Ser Gly Ile Ser Phe Arg Thr Arg Ala	
85 90 95	
cat aga gcc ctc gga tat tta ctt cac aga gtt ttt atg agg ata gct	336
His Arg Ala Leu Gly Tyr Leu Leu His Arg Val Phe Met Arg Ile Ala	
100 105 110	
ttt gat aga agc tgc agg agc ctg cgc gtc atc cga gat gcc cac ggg	384
Phe Asp Arg Ser Cys Arg Ser Leu Arg Val Ile Arg Asp Ala His Gly	
115 120 125	
ggt ctt cct tac ctt cag gtg gaa tgc cac ccc agg gac aac cct cct	432
Gly Leu Pro Tyr Leu Gln Val Glu Cys His Pro Arg Asp Asn Pro Pro	

130	135	140	
gtg gag tac ttg ttc cta cac ctt ggt tgg cga gag caa acc gat gca			480
Val Glu Tyr Leu Phe Leu His Leu Gly Trp Arg Glu Gln Thr Asp Ala			
145	150	155	160
ggc gtt tct aaa aca aat gag ccc tgg gag agc cct gaa cgc att tat			528
Gly Val Ser Lys Thr Asn Glu Pro Trp Glu Ser Pro Glu Arg Ile Tyr			
	165	170	175
tat gag cct cga ggg act ggg aag ctg cag aga ccc aaa gct gtc cga			576
Tyr Glu Pro Arg Gly Thr Gly Lys Leu Gln Arg Pro Lys Ala Val Arg			
	180	185	190
gag gac ttg gga ctt gct ctg caa aag acc tgg cct ctg ctt ttt tga			624
Glu Asp Leu Gly Leu Ala Leu Gln Lys Thr Trp Pro Leu Leu Phe *			
	195	200	205

<210> 270

<211> 207

<212> PRT

<213> Homo sapiens

<400> 270

Met Gly Arg Ile Pro Val Ile Leu Leu Leu Ala Ala Pro Pro Val Ser			
1	5	10	15
Leu Ser Ala Val Arg Leu Ala Thr Ser Ser Arg Arg Thr Lys Pro Leu			
	20	25	30
Thr Ser Phe Leu Ala Leu Gln Lys Arg Leu Gly Leu Val Pro Ser Ala			
	35	40	45
Asp Tyr Met Gln Tyr Leu Pro Ile Val Arg Arg Gly Arg Gln His Ser			
	50	55	60
Ile Val Ala Ser Thr Gln Thr Gly Arg Ala Ser Val Val Thr Ala Thr			
65	70	75	80
Tyr Ser Gly Ala Arg Asp Ile Ser Gly Ile Ser Phe Arg Thr Arg Ala			
	85	90	95
His Arg Ala Leu Gly Tyr Leu Leu His Arg Val Phe Met Arg Ile Ala			
	100	105	110
Phe Asp Arg Ser Cys Arg Ser Leu Arg Val Ile Arg Asp Ala His Gly			
	115	120	125
Gly Leu Pro Tyr Leu Gln Val Glu Cys His Pro Arg Asp Asn Pro Pro			
	130	135	140

Val Glu Tyr Leu Phe Leu His Leu Gly Trp Arg Glu Gln Thr Asp Ala
 145 150 155 160
 Gly Val Ser Lys Thr Asn Glu Pro Trp Glu Ser Pro Glu Arg Ile Tyr
 165 170 175
 Tyr Glu Pro Arg Gly Thr Gly Lys Leu Gln Arg Pro Lys Ala Val Arg
 180 185 190
 Glu Asp Leu Gly Leu Ala Leu Gln Lys Thr Trp Pro Leu Leu Phe
 195 200 205

<210> 271
 <211> 888
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(888)

<400> 271

atg gcc gga ctg ctc agt cca ata ctg ctc atg ctg ctc gca cta gtt 48
 Met Ala Gly Leu Leu Ser Pro Ile Leu Leu Met Leu Leu Ala Leu Val
 1 5 10 15

aat gtc agg acc cag aca cct cgt act aac acc ttg att gac tgc gcc 96
 Asn Val Arg Thr Gln Thr Pro Arg Thr Asn Thr Leu Ile Asp Cys Ala
 20 25 30

cct gga tgg gcg cta aaa gat cgc agt gta ggt tcg gga tcc acg tcg 144
 Pro Gly Trp Ala Leu Lys Asp Arg Ser Val Gly Ser Gly Ser Thr Ser
 35 40 45

atg ttg gca gcg cag cat atc gcc tac ccc ggg tac cag gtg ctt att 192
 Met Leu Ala Ala Gln His Ile Ala Tyr Pro Gly Tyr Gln Val Leu Ile
 50 55 60

cta gaa cgt cta atg ccc ctc acc acg gac agc cgt ctg ttt tgg agc 240
 Leu Glu Arg Leu Met Pro Leu Thr Thr Asp Ser Arg Leu Phe Trp Ser
 65 70 75 80

acg gac aag tgg atc gtc cgc ggc gaa cct tat tta aga atg agg agt 288
 Thr Asp Lys Trp Ile Val Arg Gly Glu Pro Tyr Leu Arg Met Arg Ser
 85 90 95

ttt gca tat cgc atc acc tgt ccg aaa ctc aaa tcg tat gaa caa cag	336
Phe Ala Tyr Arg Ile Thr Cys Pro Lys Leu Lys Ser Tyr Glu Gln Gln	
100 105 110	
ctg tac gaa gcg tta caa cgt ctc gta act gaa agt aac caa cac ctg	384
Leu Tyr Glu Ala Leu Gln Arg Leu Val Thr Glu Ser Asn Gln His Leu	
115 120 125	
aag gta cga cat gta cga tcg aaa tgg cat cta tat gta tcc acg cgc	432
Lys Val Arg His Val Arg Ser Lys Trp His Leu Tyr Val Ser Thr Arg	
130 135 140	
ttg tca cga cgg cat cgc acg gca cag gac gta tgc att gga gac gct	480
Leu Ser Arg Arg His Arg Thr Ala Gln Asp Val Cys Ile Gly Asp Ala	
145 150 155 160	
gca ttg acc gga tat ggt cta gac gca cgg acg cgt acg aag acg cat	528
Ala Leu Thr Gly Tyr Gly Leu Asp Ala Arg Thr Arg Thr Lys Thr His	
165 170 175	
atg tac tgt gtc gac acg tac tct gat ctg aag gca atg gta tcg act	576
Met Tyr Cys Val Asp Thr Tyr Ser Asp Leu Lys Ala Met Val Ser Thr	
180 185 190	
ctg gta cga att gtg tct gac agt cgc gtc gac ccg tat cgg att gtc	624
Leu Val Arg Ile Val Ser Asp Ser Arg Val Asp Pro Tyr Arg Ile Val	
195 200 205	
tat cga ctg cgg atc cgt att cgc atg cga tcg gct ctc acg cga ctc	672
Tyr Arg Leu Arg Ile Arg Ile Arg Met Arg Ser Ala Leu Thr Arg Leu	
210 215 220	
ata ctg cta tgg ctc gtg act gtg atg gat gcg ctt cta att cgc ggc	720
Ile Leu Leu Trp Leu Val Thr Val Met Asp Ala Leu Leu Ile Arg Gly	
225 230 235 240	
gtc tcg ctc tcg aac gac tat ctc atc tta ttc tca atc gat acg cgc	768
Val Ser Leu Ser Asn Asp Tyr Leu Ile Leu Phe Ser Ile Asp Thr Arg	
245 250 255	
acg cgt gcg aga ctc cgc atg gat cgt cta tct gct agt gta tct atg	816
Thr Arg Ala Arg Leu Arg Met Asp Arg Leu Ser Ala Ser Val Ser Met	
260 265 270	

864

888

<210> 272

<211> 295

<212> PRT

<213> Homo sapiens

<400> 272

Met Ala Gly Leu Leu Ser Pro Ile Leu Leu Met Leu Leu Ala Leu Val
1 5 10 15

Asn Val Arg Thr Gln Thr Pro Arg Thr Asn Thr Leu Ile Asp Cys Ala
20 25 30

Pro Gly Trp Ala Leu Lys Asp Arg Ser Val Gly Ser Gly Ser Thr Ser
35 40 45

Met Leu Ala Ala Gln His Ile Ala Tyr Pro Gly Tyr Gln Val Leu Ile
50 55 60

Leu Glu Arg Leu Met Pro Leu Thr Thr Asp Ser Arg Leu Phe Trp Ser
65 70 75 80

Thr Asp Lys Trp [Ile Val Arg Gly Glu Pro Tyr Leu Arg Met Arg Ser
85 90 95

Phe Ala Tyr Arg Ile Thr Cys Pro Lys Leu Lys Ser Tyr Glu Gln Gln
100 105 110

Leu Tyr Glu Ala Leu Gln Arg Leu Val Thr Glu Ser Asn Gln His Leu
115 120 125

Lys Val Arg His Val Arg Ser Lys Trp His Leu Tyr Val Ser Thr Arg
130 135 140

Leu Ser Arg Arg His Arg Thr Ala Gln Asp Val Cys Ile Gly Asp Ala
145 150 155 160

Ala Leu Thr Gly Tyr Gly Leu Asp Ala Arg Thr Arg Thr Lys Thr His
165 170 175

Met Tyr Cys Val Asp Thr Tyr Ser Asp Leu Lys Ala Met Val Ser Thr
180 185 190

Leu Val Arg Ile Val Ser Asp Ser Arg Val Asp Pro Tyr Arg Ile Val
195 200 205

Tyr Arg Leu Arg Ile Arg Ile Arg Met Arg Ser Ala Leu Thr Arg Leu

210 215 220
 Ile Leu Leu Trp Leu Val Thr Val Met Asp Ala Leu Leu Ile Arg Gly
 225 230 235 240
 Val Ser Leu Ser Asn Asp Tyr Leu Ile Leu Phe Ser Ile Asp Thr Arg
 245 250 255
 Thr Arg Ala Arg Leu Arg Met Asp Arg Leu Ser Ala Ser Val Ser Met
 260 265 270
 Leu Thr Asp Thr Ala Met Val Leu Val Thr Asp Ile Val Met Arg Ala
 275 280 285
 Val Leu Val Thr Leu His Ala
 290 295

<210> 273
 <211> 579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(579)

<400> 273
 atg ctt ctg att gag ctg ggc ttg gct gat cga gtc tgg gct cgc tca 48
 Met Leu Leu Ile Glu Leu Gly Leu Ala Asp Arg Val Trp Ala Arg Ser
 1 5 10 15
 tgt gtc tgt ggg ctg ccg gca gct cag caa ggg gct ggc tgg act agc 96
 Cys Val Cys Gly Leu Pro Ala Ala Gln Gln Gly Ala Gly Trp Thr Ser
 20 25 30
 gaa gcc atg aag cca cga agc cac ggg ctt gtc aca ggc ttt cag ggg 144
 Glu Ala Met Lys Pro Arg Ser His Gly Leu Val Thr Gly Phe Gln Gly
 35 40 45
 aca cag caa aca gta aaa gct ctg cag att caa cga agg cca gct ggg 192
 Thr Gln Gln Thr Val Lys Ala Leu Gln Ile Gln Arg Arg Pro Ala Gly
 50 55 60
 ttt gaa cca gcc atg cag ggg aac ctc cag ggt tcc ctt cga att gga 240
 Phe Glu Pro Ala Met Gln Gly Asn Leu Gln Gly Ser Leu Arg Ile Gly
 65 70 75 80
 cat tgc cat tgt ccc ctg ggt gca gat gag ggc agt gac ctg cct gag 288

His Cys His Cys Pro Leu Gly Ala Asp Glu Gly Ser Asp Leu Pro Glu
 85 90 95

gtc aca gtg ctg gtg agg gat ggc agc agg act cca cac ccg ggg gtc 336
 Val Thr Val Leu Val Arg Asp Gly Ser Arg Thr Pro His Pro Gly Val
 100 105 110

tac cca ggc tgg tac cat cgg cca gta cga ggg ctt gtc aac atg aag 384
 Tyr Pro Gly Trp Tyr His Arg Pro Val Arg Gly Leu Val Asn Met Lys
 115 120 125

gtt cca ttt gtc agg ccc ctg cat gag gac ccc aac ccc ctg aag atc 432
 Val Pro Phe Val Arg Pro Leu His Glu Asp Pro Asn Pro Leu Lys Ile
 130 135 140

ttc atg tta agt gct gct ggc aac aaa agt aga tgg atc cct gga agt 480
 Phe Met Leu Ser Ala Ala Gly Asn Lys Ser Arg Trp Ile Pro Gly Ser
 145 150 155 160

ctc tgt ctg cac gtg aca gct act cca acc act gct gag ctt cca gga 528
 Leu Cys Leu His Val Thr Ala Thr Pro Thr Thr Ala Glu Leu Pro Gly
 165 170 175

gct tcc cgt gat ggc aag gta cca gct gtg tgc cga gta cca gct gtg 576
 Ala Ser Arg Asp Gly Lys Val Pro Ala Val Cys Arg Val Pro Ala Val
 180 185 190

tga 579
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<210> 274

<211> 192

<212> PRT

<213> Homo sapiens

<400> 274

Met Leu Leu Ile Glu Leu Gly Leu Ala Asp Arg Val Trp Ala Arg Ser
 1 5 10 15

Cys Val Cys Gly Leu Pro Ala Ala Gln Gln Gly Ala Gly Trp Thr Ser
 20 25 30

Glu Ala Met Lys Pro Arg Ser His Gly Leu Val Thr Gly Phe Gln Gly

35 40 45
 Thr Gln Gln Thr Val Lys Ala Leu Gln Ile Gln Arg Arg Pro Ala Gly
 50 55 60
 Phe Glu Pro Ala Met Gln Gly Asn Leu Gln Gly Ser Leu Arg Ile Gly
 65 70 75 80
 His Cys His Cys Pro Leu Gly Ala Asp Glu Gly Ser Asp Leu Pro Glu
 85 90 95
 Val Thr Val Leu Val Arg Asp Gly Ser Arg Thr Pro His Pro Gly Val
 100 105 110
 Tyr Pro Gly Trp Tyr His Arg Pro Val Arg Gly Leu Val Asn Met Lys
 115 120 125
 Val Pro Phe Val Arg Pro Leu His Glu Asp Pro Asn Pro Leu Lys Ile
 130 135 140
 Phe Met Leu Ser Ala Ala Gly Asn Lys Ser Arg Trp Ile Pro Gly Ser
 145 150 155 160
 Leu Cys Leu His Val Thr Ala Thr Pro Thr Thr Ala Glu Leu Pro Gly
 165 170 175
 Ala Ser Arg Asp Gly Lys Val Pro Ala Val Cys Arg Val Pro Ala Val
 180 185 190

<210> 275

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(510)

<400> 275

atg agg tca gaa gcc ttg ctg cta tat ttc aca ctg cta cac ttt gct 48
 Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1 5 10 15

ggg gct ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc 96
 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 20 25 30

aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg 144
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 35 40 45

aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg 192

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60
 aac gga acc ctc tac att gct gct agg aca cag aga ggc ttt gtt gtc 240
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Thr Gln Arg Gly Phe Val Val
 65 70 75 80
 ttt gtg gtc acc ggg tcc act tta cac aga tgc cta tta atc act tca 288
 Phe Val Val Thr Gly Ser Thr Leu His Arg Cys Leu Leu Ile Thr Ser
 85 90 95
 cta tgg aga cag aca cat cca tca tat cac agc agc tca gaa acg ggc 336
 Leu Trp Arg Gln Thr His Pro Ser Tyr His Ser Ser Ser Glu Thr Gly
 100 105 110
 cgt cca gtg aaa ggg ggt gag agg gga aag tgc aca ctt aac cat ttc 384
 Arg Pro Val Lys Gly Gly Glu Arg Gly Lys Cys Thr Leu Asn His Phe
 115 120 125
 gag tta ggt tac tgg ttg cct gtg tct tac acg ctt agg gtg gta att 432
 Glu Leu Gly Tyr Trp Leu Pro Val Ser Tyr Thr Leu Arg Val Val Ile
 130 135 140
 ggg gtg ggg act ctg gag tat gct tat tct tca tcc aag aaa aag cag 480
 Gly Val Gly Thr Leu Glu Tyr Ala Tyr Ser Ser Ser Lys Lys Lys Gln
 145 150 155 160
 agt tgg cac tac tgt gag aaa agt act taa 510
 Ser Trp His Tyr Cys Glu Lys Ser Thr *
 165

<210> 276

<211> 169

<212> PRT

<213> Homo sapiens

<400> 276

Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1 5 10 15
 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 20 25 30
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg

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<210> 277
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(423)
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<400> 277																
atg	tcc	acc	acc	aca	tgc	caa	gtg	gtg	gcg	ttc	ctc	ctg	tcc	atc	ctg	48
Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile	Leu	
1				5					10					15		
ggg	ctg	gcc	ggc	tgc	atc	gcg	gcc	acc	ggg	atg	gac	atg	tgg	agc	acc	96
Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp	Ser	Thr	
			20					25					30			
cag	gac	ctg	tac	gac	aac	ccc	gtc	acc	tcc	gtg	ttc	cag	tac	gaa	ggg	144
Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln	Tyr	Glu	Gly	
		35					40					45				
ctc	tgg	agg	agc	tgc	gtg	agg	cag	agt	tca	ggc	ttc	acc	gaa	tgc	agg	192
Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe	Thr	Glu	Cys	Arg	
	50					55					60					

<400> 278															
Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile	Leu
1				5					10					15	
Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp	Ser	Thr
			20					25					30		
Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln	Tyr	Glu	Gly
		35					40					45			
Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe	Thr	Glu	Cys	Arg
	50					55					60				
Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Val	Ser	Tyr	Ser	Pro	Ile	Leu
65					70					75					80
Phe	Leu	Leu	Ser	Phe	Gln	Tyr	Thr	Leu	Asp	Leu	Val	Leu	Asp	Ile	His
				85					90					95	
Cys	Ser	Cys	Ser	Pro	Glu	Phe	Pro	Pro	Pro	Pro	Pro	Gln	Leu	Ser	Ser
			100					105					110		
His	Lys	Ser	Ser	Ser	Lys	Pro	Pro	Gln	Ala	Pro	Lys	Leu	Asn	Lys	Asp

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<210> 279
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(333)

<400> 279
atg atg ctg ctg ttg ctg tgt ctg ggg ttg acc ctc gtc tgt gcc cag      48
Met Met Leu Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys Ala Gln
 1                5                10                15

gag gaa gaa aac aat gat gct gtg aca agc aac ttc gat ctg tca aag      96
Glu Glu Glu Asn Asn Asp Ala Val Thr Ser Asn Phe Asp Leu Ser Lys
      20                25                30

cac att gct cag gat ata gca tca att cga aca ccg gat gtg agc tca     144
His Ile Ala Gln Asp Ile Ala Ser Ile Arg Thr Pro Asp Val Ser Ser
      35                40                45

caa ctc aag gag agg ttt gtg aaa tat tgt gaa gaa cat ggg att gat     192
Gln Leu Lys Glu Arg Phe Val Lys Tyr Cys Glu Glu His Gly Ile Asp
      50                55                60

aag gaa aac ata ttt gac ttg acc aaa gtt gga ttc tct gct gaa atc     240
Lys Glu Asn Ile Phe Asp Leu Thr Lys Val Gly Phe Ser Ala Glu Ile
      65                70                75                80

atg cgg gcc gat tcg cgg tct cga tgt tta acc gtg ctg gta aca cca     288
Met Arg Ala Asp Ser Arg Ser Arg Cys Leu Thr Val Leu Val Thr Pro
      85                90                95

aac ctc gat gct tgc gac gac ttg gtg cac ata ttg ttc gac tag       333
Asn Leu Asp Ala Cys Asp Asp Leu Val His Ile Leu Phe Asp *
      100                105                110

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<400> 280

<210> 281

<211> 471

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(471)

<400> 281

atg	aaa	ata	agc	tgc	tca	gat	ctt	ctg	ctg	cag	gga	gca	aag	ttg	atg	48
Met	Lys	Ile	Ser	Cys	Ser	Asp	Leu	Leu	Leu	Gln	Gly	Ala	Lys	Leu	Met	
1				5					10					15		
atg	gtt	cca	gct	gac	tcc	ctt	ctg	gat	tta	ctg	ctg	tta	acc	tgc	ctt	96
Met	Val	Pro	Ala	Asp	Ser	Leu	Leu	Asp	Leu	Leu	Leu	Leu	Thr	Cys	Leu	
			20					25					30			
cct	cag	gca	gga	gag	tct	cga	gta	gaa	ggc	aaa	gat	acc	cct	gcc	tcg	144
Pro	Gln	Ala	Gly	Glu	Ser	Arg	Val	Glu	Gly	Lys	Asp	Thr	Pro	Ala	Ser	
		35					40					45				

cct gaa cat aaa gcg gat gcg cac atc gtt aag atc cac gtg ata gag 192
 Pro Glu His Lys Ala Asp Ala His Ile Val Lys Ile His Val Ile Glu
 50 55 60

ata aat cct cga ttt aat cta ggc ggg agt gat gcg ttt ctt gtg agc 240
 Ile Asn Pro Arg Phe Asn Leu Gly Gly Ser Asp Ala Phe Leu Val Ser
 65 70 75 80

ccg att cgg caa gat tta cgt ggg cag gtc ctt tct ata ttc gag ctg 288
 Pro Ile Arg Gln Asp Leu Arg Gly Gln Val Leu Ser Ile Phe Glu Leu
 85 90 95

acc caa agc acc tta tca gat gaa agg att act cag cat caa cat tta 336
 Thr Gln Ser Thr Leu Ser Asp Glu Arg Ile Thr Gln His Gln His Leu
 100 105 110

cat agt aga ggt gag cta tct tgt gaa ccg gat gtg gag ccc tta ggc 384
 His Ser Arg Gly Glu Leu Ser Cys Glu Pro Asp Val Glu Pro Leu Gly
 115 120 125

ttc agc gcc cgg aaa ggt caa tgc ctc cgt agg gac cac agt cag att 432
 Phe Ser Ala Arg Lys Gly Gln Cys Leu Arg Arg Asp His Ser Gln Ile
 130 135 140

gca act cct cct tcg gta aat gcc gaa aaa aca acg tag 471
 Ala Thr Pro Pro Ser Val Asn Ala Glu Lys Thr Thr *
 145 150 155

<210> 282

<211> 156

<212> PRT

<213> Homo sapiens

<400> 282

Met Lys Ile Ser Cys Ser Asp Leu Leu Leu Gln Gly Ala Lys Leu Met
 1 5 10 15
 Met Val Pro Ala Asp Ser Leu Leu Asp Leu Leu Leu Leu Thr Cys Leu
 20 25 30
 Pro Gln Ala Gly Glu Ser Arg Val Glu Gly Lys Asp Thr Pro Ala Ser
 35 40 45
 Pro Glu His Lys Ala Asp Ala His Ile Val Lys Ile His Val Ile Glu
 50 55 60

Ile Asn Pro Arg Phe Asn Leu Gly Gly Ser Asp Ala Phe Leu Val Ser
 65 70 75 80
 Pro Ile Arg Gln Asp Leu Arg Gly Gln Val Leu Ser Ile Phe Glu Leu
 85 90 95
 Thr Gln Ser Thr Leu Ser Asp Glu Arg Ile Thr Gln His Gln His Leu
 100 105 110
 His Ser Arg Gly Glu Leu Ser Cys Glu Pro Asp Val Glu Pro Leu Gly
 115 120 125
 Phe Ser Ala Arg Lys Gly Gln Cys Leu Arg Arg Asp His Ser Gln Ile
 130 135 140
 Ala Thr Pro Pro Ser Val Asn Ala Glu Lys Thr Thr
 145 150 155

<210> 283
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(702)

<400> 283

atg gaa ggc tcc att tat gct tgg ggc att ctc ttg atg ttg ggc gcg	48
Met Glu Gly Ser Ile Tyr Ala Trp Gly Ile Leu Leu Met Leu Gly Ala	
1 5 10 15	
gtt cct ccg ggg tgg tgt ggg ggt gtg ttg aaa tct gct cga cgt ccg	96
Val Pro Pro Gly Trp Cys Gly Gly Val Leu Lys Ser Ala Arg Pro	
20 25 30	
gag aag gct acg gcc gtt gtg cta cat gag gag tgt atg cgt aaa cat	144
Glu Lys Ala Thr Ala Val Val Leu His Glu Glu Cys Met Arg Lys His	
35 40 45	
ctt gcg gct aaa ccg acc gct cta att tta aaa agg cat cgg caa gca	192
Leu Ala Ala Lys Pro Thr Ala Leu Ile Leu Lys Arg His Arg Gln Ala	
50 55 60	
ggc gcc cac aag tcg agt tac ccg ggt caa caa agc tca gcg cct acc	240
Gly Ala His Lys Ser Ser Tyr Pro Gly Gln Gln Ser Ser Ala Pro Thr	
65 70 75 80	

ttc gag aga gga cgg ctt cgc atc ggt gca cca gca act cca caa tac	288
Phe Glu Arg Gly Arg Leu Arg Ile Gly Ala Pro Ala Thr Pro Gln Tyr	
85 90 95	
atg aaa gta agc cgg ttc acc aga ccc cag ccc agt ctc caa gtt gca	336
Met Lys Val Ser Arg Phe Thr Arg Pro Gln Pro Ser Leu Gln Val Ala	
100 105 110	
cag cat gta aat tca gcc acc aag ttc ccc tgc agg gct ttt ggg acc	384
Gln His Val Asn Ser Ala Thr Lys Phe Pro Cys Arg Ala Phe Gly Thr	
115 120 125	
tat ctt cag gtg gtc gac aag gct tgg aac tct cgc tgg cag act agt	432
Tyr Leu Gln Val Val Asp Lys Ala Trp Asn Ser Arg Trp Gln Thr Ser	
130 135 140	
att gtc ata ata cct gga ccc acg ggc atg aac gcc tca cca tca cat	480
Ile Val Ile Ile Pro Gly Pro Thr Gly Met Asn Ala Ser Pro Ser His	
145 150 155 160	
ccg agt cag ctt tgc gcg gcg tct gaa tcg gtc cgg cat cgg tta cgc	528
Pro Ser Gln Leu Cys Ala Ala Ser Glu Ser Val Arg His Arg Leu Arg	
165 170 175	
att ggg cgc ctg ccc gcc gcc aag ggt tta gct tcg ctc atg tca aga	576
Ile Gly Arg Leu Pro Ala Ala Lys Gly Leu Ala Ser Leu Met Ser Arg	
180 185 190	
cgt ctt cgt ccg atg act gga act aca gct gaa gtg tcg tca aaa atc	624
Arg Leu Arg Pro Met Thr Gly Thr Thr Ala Glu Val Ser Ser Lys Ile	
195 200 205	
atc agg gat ggg gga gca gaa cgt ccc ggg gga ccg cgg ctc cca act	672
Ile Arg Asp Gly Gly Ala Glu Arg Pro Gly Gly Pro Arg Leu Pro Thr	
210 215 220	
cac gtt gct ccc act ccg aga ctc aag taa	702
His Val Ala Pro Thr Pro Arg Leu Lys *	
225 230	

<210> 284

<211> 233

<212> PRT

<213> Homo sapiens

<400> 284

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Met Glu Gly Ser Ile Tyr Ala Trp Gly Ile Leu Leu Met Leu Gly Ala
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Val Pro Pro Gly Trp Cys Gly Gly Val Leu Lys Ser Ala Arg Arg Pro
          20           25           30
Glu Lys Ala Thr Ala Val Val Leu His Glu Glu Cys Met Arg Lys His
          35           40           45
Leu Ala Ala Lys Pro Thr Ala Leu Ile Leu Lys Arg His Arg Gln Ala
          50           55           60
Gly Ala His Lys Ser Ser Tyr Pro Gly Gln Gln Ser Ser Ala Pro Thr
65           70           75           80
Phe Glu Arg Gly Arg Leu Arg Ile Gly Ala Pro Ala Thr Pro Gln Tyr
          85           90           95
Met Lys Val Ser Arg Phe Thr Arg Pro Gln Pro Ser Leu Gln Val Ala
          100          105          110
Gln His Val Asn Ser Ala Thr Lys Phe Pro Cys Arg Ala Phe Gly Thr
          115          120          125
Tyr Leu Gln Val Val Asp Lys Ala Trp Asn Ser Arg Trp Gln Thr Ser
          130          135          140
Ile Val Ile Ile Pro Gly Pro Thr Gly Met Asn Ala Ser Pro Ser His
          145          150          155          160
Pro Ser Gln Leu Cys Ala Ala Ser Glu Ser Val Arg His Arg Leu Arg
          165          170          175
Ile Gly Arg Leu Pro Ala Ala Lys Gly Leu Ala Ser Leu Met Ser Arg
          180          185          190
Arg Leu Arg Pro Met Thr Gly Thr Thr Ala Glu Val Ser Ser Lys Ile
          195          200          205
Ile Arg Asp Gly Gly Ala Glu Arg Pro Gly Gly Pro Arg Leu Pro Thr
          210          215          220
His Val Ala Pro Thr Pro Arg Leu Lys
          225          230

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<210> 285

<211> 369

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(369)

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<400> 285
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 Met Pro Cys Ala Leu Trp Glu His Lys Asn Lys Val Arg Leu Ser Pro
 1 5 10 15

 ctc tca tcg ttg tta ctg ttg ctt cat cca gga tat ggt gga cag tca 96
 Leu Ser Ser Leu Leu Leu Leu Leu His Pro Gly Tyr Gly Gly Gln Ser
 20 25 30

 gaa tcc gaa agc ttg cag caa aat ggc tgg ctt tac ctt att ttg gag 144
 Glu Ser Glu Ser Leu Gln Gln Asn Gly Trp Leu Tyr Leu Ile Leu Glu
 35 40 45

 gga ata tat ttt ctg aaa gtt cag gcc tgg gta att cca aat gac aat 192
 Gly Ile Tyr Phe Leu Lys Val Gln Ala Trp Val Ile Pro Asn Asp Asn
 50 55 60

 ctg aat aga atg tta ttg gca gaa gtg aac aaa tat gaa aat gtt ctc 240
 Leu Asn Arg Met Leu Leu Ala Glu Val Asn Lys Tyr Glu Asn Val Leu
 65 70 75 80

 gta att aag gtc cta gga gag tta cat ggg aca ccc aag agt gct tat 288
 Val Ile Lys Val Leu Gly Glu Leu His Gly Thr Pro Lys Ser Ala Tyr
 85 90 95

 gag aaa gtt tgg ggc att gct gat agc aat cag aat cag aaa tgt acc 336
 Glu Lys Val Trp Gly Ile Ala Asp Ser Asn Gln Asn Gln Lys Cys Thr
 100 105 110

 tgc tca gat tat cca tat aaa caa ttg aaa taa 369
 Cys Ser Asp Tyr Pro Tyr Lys Gln Leu Lys *
 115 120

<210> 286

<211> 122

<212> PRT

<213> Homo sapiens

<400> 286

Met Pro Cys Ala Leu Trp Glu His Lys Asn Lys Val Arg Leu Ser Pro
 1 5 10 15

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<210> 287
<211> 486
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(486)
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<400> 287

atg	ggg	aaa	ctc	ttg	act	ttg	gtc	agc	atg	ctc	cta	agt	gga	ctg	cag	48
Met	Gly	Lys	Leu	Leu	Thr	Leu	Val	Ser	Met	Leu	Leu	Ser	Gly	Leu	Gln	
1				5					10					15		
gct	atg	tgg	gaa	ctg	gtg	tat	aga	act	att	ggg	cac	caa	ctt	cac	tgg	96
Ala	Met	Trp	Glu	Leu	Val	Tyr	Arg	Thr	Ile	Gly	His	Gln	Leu	His	Trp	
			20					25					30			
atc	agt	ggc	tat	ata	gcg	acg	gtt	gta	cga	ggg	ttt	cgc	cac	gtc	aca	144
Ile	Ser	Gly	Tyr	Ile	Ala	Thr	Val	Val	Arg	Gly	Phe	Arg	His	Val	Thr	
		35					40					45				
caa	ggt	gat	tgc	aaa	cat	tat	gtg	atc	ctc	aca	aac	aca	ggt	tgt	atc	192
Gln	Gly	Asp	Cys	Lys	His	Tyr	Val	Ile	Leu	Thr	Asn	Thr	Gly	Cys	Ile	
	50					55					60					
tgt	ggt	gga	caa	gtt	atg	tgg	act	gta	cct	tat	tgt	tat	cct	ggt	gtg	240
Cys	Gly	Gly	Gln	Val	Met	Trp	Thr	Val	Pro	Tyr	Cys	Tyr	Pro	Gly	Val	

65	70	75	80	
tca tca gtt ggt tgc att aac tgt ctt ccc att ttg tct cca ttg agg				288
Ser Ser Val Gly Cys Ile Asn Cys Leu Pro Ile Leu Ser Pro Leu Arg				
	85	90	95	
tta agt aac cta tgt gtt tta ttc aac gca atg aga ggg aga cgt aac				336
Leu Ser Asn Leu Cys Val Leu Phe Asn Ala Met Arg Gly Arg Arg Asn				
	100	105	110	
aag gtg ttt gtt tca ccc gag gac cta aca cgg ctc ggg gga gag aag				384
Lys Val Phe Val Ser Pro Glu Asp Leu Thr Arg Leu Gly Gly Glu Lys				
	115	120	125	
gga ggt acc aga aga gcg gaa gag gga aga gag aca gaa aag gag cat				432
Gly Gly Thr Arg Arg Ala Glu Glu Gly Arg Glu Thr Glu Lys Glu His				
	130	135	140	
ata gaa gat cgg aag agg aaa agg aga aag gaa ata gtc aac aag gaa				480
Ile Glu Asp Arg Lys Arg Lys Arg Arg Lys Glu Ile Val Asn Lys Glu				
	145	150	155	160
aaa tag				486
Lys *				

<210> 288

<211> 161

<212> PRT

<213> Homo sapiens

<400> 288

Met Gly Lys Leu Leu Thr Leu Val Ser Met Leu Leu Ser Gly Leu Gln				
1	5	10	15	
Ala Met Trp Glu Leu Val Tyr Arg Thr Ile Gly His Gln Leu His Trp				
20	25	30		
Ile Ser Gly Tyr Ile Ala Thr Val Val Arg Gly Phe Arg His Val Thr				
35	40	45		
Gln Gly Asp Cys Lys His Tyr Val Ile Leu Thr Asn Thr Gly Cys Ile				
50	55	60		
Cys Gly Gly Gln Val Met Trp Thr Val Pro Tyr Cys Tyr Pro Gly Val				
65	70	75	80	

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<210> 289
<211> 651
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(651)
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<400> 289																
atg	agg	ggc	acc	cac	atc	ctc	atg	ggg	ctg	agt	ctc	ttc	tat	ccc	atc	48
Met	Arg	Gly	Thr	His	Ile	Leu	Met	Gly	Leu	Ser	Leu	Phe	Tyr	Pro	Ile	
1			5			10			15							
aga	gcc	ctg	gaa	aca	ggg	acc	caa	gtg	gtc	tgc	ggc	cac	cag	ccc	tgg	96
Arg	Ala	Leu	Glu	Thr	Gly	Thr	Gln	Val	Val	Cys	Gly	His	Gln	Pro	Trp	
20			25			30										
tgt	ggc	ctg	aag	gct	ggg	cgt	cta	ggc	ctc	cgg	cct	cca	ccc	cct	ctg	144
Cys	Gly	Leu	Lys	Ala	Gly	Arg	Leu	Gly	Leu	Arg	Pro	Pro	Pro	Pro	Leu	
35			40			45										
tgc	agt	ggg	cag	tca	cac	ctg	gcg	ggg	ccc	ggc	tgc	ctg	ccc	aga	cag	192
Cys	Ser	Gly	Gln	Ser	His	Leu	Ala	Gly	Pro	Gly	Cys	Leu	Pro	Arg	Gln	
50			55			60										
cag	gtt	ctc	agc	agc	agc	cct	ggc	gtc	cca	gga	gag	ggg	ctt	ctc	tct	240
Gln	Val	Leu	Ser	Ser	Ser	Pro	Gly	Val	Pro	Gly	Glu	Gly	Leu	Leu	Ser	
65			70			75			80							

Met Arg Gly Thr His Ile Leu Met Gly Leu Ser Leu Phe Tyr Pro Ile
 1 5 10 15
 Arg Ala Leu Glu Thr Gly Thr Gln Val Val Cys Gly His Gln Pro Trp
 20 25 30
 Cys Gly Leu Lys Ala Gly Arg Leu Gly Leu Arg Pro Pro Pro Pro Leu
 35 40 45
 Cys Ser Gly Gln Ser His Leu Ala Gly Pro Gly Cys Leu Pro Arg Gln
 50 55 60
 Gln Val Leu Ser Ser Ser Pro Gly Val Pro Gly Glu Gly Leu Leu Ser
 65 70 75 80
 Ala Pro Gly Phe Gln Glu His Arg Asp Ala Trp Val Cys Ser His Asp
 85 90 95
 Leu Gly Ser Cys Ile Cys Ala Gln Arg Gly Gly Ala Pro Ala Cys Ser
 100 105 110
 Met Glu Gln Lys Ala Trp Ile Cys Ser Trp Asp Leu Gly Gly Ala Ser
 115 120 125
 Ala Cys Ser Val Glu Gln Glu Val Trp Val Tyr Ser Cys Asp Phe Ser
 130 135 140
 Gly Cys Ser Cys Ala Gln Glu Ser Gly Ala Pro Ile Cys Ser Arg Pro
 145 150 155 160
 Glu Ser Thr Gly Met Pro Lys Ser Ala Glu Ser Tyr His Pro Pro Arg
 165 170 175
 Lys Gly Gln Gly Leu Cys Leu Ser Ala Ala Pro Ala Ser Ser Met Glu
 180 185 190
 His Ala Ala Leu Ala Val Ala Ala Cys Cys Ser Trp His Asp Gly Thr
 195 200 205
 Ser His Phe Arg Trp Thr Arg Val
 210 215

<210> 291

<211> 708

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(708)

<400> 291

atg cgg cct gat gac att aac ccg agg act ggg ctg gtg gtg gcc ctg
 Met Arg Pro Asp Asp Ile Asn Pro Arg Thr Gly Leu Val Val Ala Leu
 1 5 10 15

[illegible]

gag gat agc atc ttc ttt gtg ccc cag gac agt atc atc gtt tgc tcc 624
 Glu Asp Ser Ile Phe Phe Val Pro Gln Asp Ser Ile Ile Val Cys Ser
 195 200 205

 tac aag cag aac agc ccg tat gac aga tac tgt tgt tat atc aat cag 672
 Tyr Lys Gln Asn Ser Pro Tyr Asp Arg Tyr Cys Cys Tyr Ile Asn Gln
 210 215 220

 ata caa ggc agg tgg gac cac gag acc atc gtc taa 708
 Ile Gln Gly Arg Trp Asp His Glu Thr Ile Val *
 225 230 235

<210> 292
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 292
 Met Arg Pro Asp Asp Ile Asn Pro Arg Thr Gly Leu Val Val Ala Leu
 1 5 10 15
 Val Ser Val Phe Leu Val Phe Gly Phe Met Phe Thr Val Ser Gly Met
 20 25 30
 Lys Gly Glu Thr Leu Gly Asn Ile Pro Leu Leu Ala Ile Gly Pro Ala
 35 40 45
 Ile Cys Leu Pro Gly Ile Ala Ala Ile Ala Leu Ala Arg Lys Thr Glu
 50 55 60
 Gly Cys Thr Lys Trp Pro Glu Asn Glu Leu Leu Trp Val Arg Lys Leu
 65 70 75 80
 Pro Cys Phe Arg Lys Pro Lys Asp Lys Glu Val Val Glu Leu Leu Arg
 85 90 95
 Thr Pro Ser Asp Leu Glu Ser Gly Lys Gly Ser Ser Asp Glu Leu Ala
 100 105 110
 Lys Lys Ala Gly Leu Arg Gly Lys Pro Pro Pro Gln Ser Gln Gly Glu
 115 120 125
 Val Ser Val Ala Ser Ser Ile Asn Ser Pro Thr Pro Thr Glu Glu Gly
 130 135 140
 Glu Cys Gln Ser Leu Val Gln Asn Gly His Gln Glu Glu Thr Ser Arg
 145 150 155 160
 Tyr Leu Asp Gly Tyr Cys Pro Ser Gly Ser Ser Leu Thr Tyr Ser Ala
 165 170 175
 Leu Asp Val Lys Cys Ser Ala Arg Asp Arg Ser Glu Cys Pro Glu Pro

180 185 190
 Glu Asp Ser Ile Phe Phe Val Pro Gln Asp Ser Ile Ile Val Cys Ser
 195 200 205
 Tyr Lys Gln Asn Ser Pro Tyr Asp Arg Tyr Cys Cys Tyr Ile Asn Gln
 210 215 220
 Ile Gln Gly Arg Trp Asp His Glu Thr Ile Val
 225 230 235

<210> 293
 <211> 822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(822)

<400> 293

atg gtg gac ccc acc ggc ttc cgg gag atc gtg gct gcc aat cct ctg	48
Met Val Asp Pro Thr Gly Phe Arg Glu Ile Val Ala Ala Asn Pro Leu	
1 5 10 15	
ctc ctc acg ggc gcc tac atc ctc ctg gcc atg ggg ggc ctg ctc ttt	96
Leu Leu Thr Gly Ala Tyr Ile Leu Leu Ala Met Gly Gly Leu Leu Phe	
20 25 30	
ctg ctc ggc ttc ctg ggc tgc tgc ggg gcc gtc cgt gag aac aag tgt	144
Leu Leu Gly Phe Leu Gly Cys Cys Gly Ala Val Arg Glu Asn Lys Cys	
35 40 45	
ctg ctg cta ttt ctt cct caa ctt cga aaa ggg gaa act aca caa aaa	192
Leu Leu Leu Phe Leu Pro Gln Leu Arg Lys Gly Glu Thr Thr Gln Lys	
50 55 60	
aga gac cgt gag aac agc gtc cgg tgc ccg gcg gtc ccc tgt gag agc	240
Arg Asp Arg Glu Asn Ser Val Arg Cys Pro Ala Val Pro Cys Glu Ser	
65 70 75 80	
aga agc ctg tgt cgg agc cgc tgg agc cca ttc ttc ctg ttc atc ctg	288
Arg Ser Leu Cys Arg Ser Arg Trp Ser Pro Phe Phe Leu Phe Ile Leu	
85 90 95	
atc atc ttc ctg gca gag ctc tca gca gcc atc ctg gcc ttc atc ttc	336

Ile Ile Phe Leu Ala Glu Leu Ser Ala Ala Ile Leu Ala Phe Ile Phe
 100 105 110

agg gaa aat gta cgt atc agg ccc caa gct ttc ctg cct cct gct atc 384
 Arg Glu Asn Val Arg Ile Arg Pro Gln Ala Phe Leu Pro Pro Ala Ile
 115 120 125

agc aag ggg ttg gtg gcc att cag ctc acc cga gaa ttc ttc acc aag 432
 Ser Lys Gly Leu Val Ala Ile Gln Leu Thr Arg Glu Phe Phe Thr Lys
 130 135 140

gag ctc acc aag cac tac cag ggc aat aac gac aca gac gtc ttc tct 480
 Glu Leu Thr Lys His Tyr Gln Gly Asn Asn Asp Thr Asp Val Phe Ser
 145 150 155 160

gcc acc tgg aac tcg gtc atg atc aca ttt ggt tgc tgc ggg gtc aac 528
 Ala Thr Trp Asn Ser Val Met Ile Thr Phe Gly Cys Cys Gly Val Asn
 165 170 175

ggg cct gaa gac ttt aag ttt gca tct gtg ttt cga ctc ctg acc ctg 576
 Gly Pro Glu Asp Phe Lys Phe Ala Ser Val Phe Arg Leu Leu Thr Leu
 180 185 190

gat agt gaa gag gtg ccg gag gcc tgc tgc cgg agg gaa ccc caa agt 624
 Asp Ser Glu Glu Val Pro Glu Ala Cys Cys Arg Arg Glu Pro Gln Ser
 195 200 205

cgg gac ggg gtc ctg ctg agc cgg gag gag tgc ctc ctg gga agg agc 672
 Arg Asp Gly Val Leu Leu Ser Arg Glu Glu Cys Leu Leu Gly Arg Ser
 210 215 220

cta ttc cta aac aag cag ggc tgt tac acg gtg atc ctc aac acc ttc 720
 Leu Phe Leu Asn Lys Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe
 225 230 235 240

gag acc tac gtc tac ttg gcc gga gcc ctt gcc atc ggg gta ctg gcc 768
 Glu Thr Tyr Val Tyr Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala
 245 250 255

atc gag ctt ttc gcc atg atc ttt gcc atg tgc ctc ttc cgg ggc atc 816
 Ile Glu Leu Phe Ala Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile
 260 265 270

822

<400> 294															
Met 1	Val	Asp	Pro	Thr	Gly	Phe	Arg	Glu	Ile	Val	Ala	Ala	Asn	Pro	Leu
				5				10					15		
Leu	Leu	Thr	Gly	Ala	Tyr	Ile	Leu	Leu	Ala	Met	Gly	Gly	Leu	Leu	Phe
			20					25					30		
Leu	Leu	Gly	Phe	Leu	Gly	Cys	Cys	Gly	Ala	Val	Arg	Glu	Asn	Lys	Cys
		35				40						45			
Leu	Leu	Leu	Phe	Leu	Pro	Gln	Leu	Arg	Lys	Gly	Glu	Thr	Thr	Gln	Lys
		50				55					60				
Arg	Asp	Arg	Glu	Asn	Ser	Val	Arg	Cys	Pro	Ala	Val	Pro	Cys	Glu	Ser
65					70					75				80	
Arg	Ser	Leu	Cys	Arg	Ser	Arg	Trp	Ser	Pro	Phe	Phe	Leu	Phe	Ile	Leu
				85					90					95	
Ile	Ile	Phe	Leu	Ala	Glu	Leu	Ser	Ala	Ala	Ile	Leu	Ala	Phe	Ile	Phe
			100					105					110		
Arg	Glu	Asn	Val	Arg	Ile	Arg	Pro	Gln	Ala	Phe	Leu	Pro	Pro	Ala	Ile
		115					120					125			
Ser	Lys	Gly	Leu	Val	Ala	Ile	Gln	Leu	Thr	Arg	Glu	Phe	Phe	Thr	Lys
		130				135					140				
Glu	Leu	Thr	Lys	His	Tyr	Gln	Gly	Asn	Asn	Asp	Thr	Asp	Val	Phe	Ser
145					150					155				160	
Ala	Thr	Trp	Asn	Ser	Val	Met	Ile	Thr	Phe	Gly	Cys	Cys	Gly	Val	Asn
				165					170					175	
Gly	Pro	Glu	Asp	Phe	Lys	Phe	Ala	Ser	Val	Phe	Arg	Leu	Leu	Thr	Leu
			180					185					190		
Asp	Ser	Glu	Glu	Val	Pro	Glu	Ala	Cys	Cys	Arg	Arg	Glu	Pro	Gln	Ser
		195					200					205			
Arg	Asp	Gly	Val	Leu	Leu	Ser	Arg	Glu	Glu	Cys	Leu	Leu	Gly	Arg	Ser
		210				215					220				
Leu	Phe	Leu	Asn	Lys	Gln	Gly	Cys	Tyr	Thr	Val	Ile	Leu	Asn	Thr	Phe
225					230					235				240	
Glu	Thr	Tyr	Val	Tyr	Leu	Ala	Gly	Ala	Leu	Ala	Ile	Gly	Val	Leu	Ala
				245					250					255	

Ile Glu Leu Phe Ala Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile
 260 265 270
 Gln

<210> 295
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 295
 atg agc aga gac cac agg ctg ctg tgc ctc ctg ggc ctc tgt tgt gtg 48
 Met Ser Arg Asp His Arg Leu Leu Cys Leu Leu Gly Leu Cys Cys Val
 1 5 10 15
 gca gat gct tcc aaa cag ccc ttc agg aaa tct gga att ccc aga ggt 96
 Ala Asp Ala Ser Lys Gln Pro Phe Arg Lys Ser Gly Ile Pro Arg Gly
 20 25 30
 tat aca ttg cac ctg agg cca tct ggc tac aat cca aac tct ggg tgc 144
 Tyr Thr Leu His Leu Arg Pro Ser Gly Tyr Asn Pro Asn Ser Gly Cys
 35 40 45
 ggc tgg cgc caa agc tac tac acc atg ctg cct tct aag ctg cat ttc 192
 Gly Trp Arg Gln Ser Tyr Tyr Thr Met Leu Pro Ser Lys Leu His Phe
 50 55 60
 atc tgg aac cgc tgt ggc tgg cag gcc gag cct ctg aac act gca att 240
 Ile Trp Asn Arg Cys Gly Trp Gln Ala Glu Pro Leu Asn Thr Ala Ile
 65 70 75 80
 cag gtt aat cat gca gac ctg ctg gag cac gcg ggg ccg agg gga ggc 288
 Gln Val Asn His Ala Asp Leu Leu Glu His Ala Gly Pro Arg Gly Gly
 85 90 95
 cca cac tac cgc ttt ccc cac tct ggg gac ggg gag aac ctg att tgt 336
 Pro His Tyr Arg Phe Pro His Ser Gly Asp Gly Glu Asn Leu Ile Cys
 100 105 110

"222" 222560

ctt cgg tcc aca gct agt gtg tgc aag ggc cca att cag gtc cag atc 384
 Leu Arg Ser Thr Ala Ser Val Cys Lys Gly Pro Ile Gln Val Gln Ile
 115 120 125

ggc gtg ctg aca agg act gtg ttt ggg gct gct ccc ctg cag aca gag 432
 Gly Val Leu Thr Arg Thr Val Phe Gly Ala Ala Pro Leu Gln Thr Glu
 130 135 140

ccc cat ggg cag gcc ctg atg ggc ggt cag agg aca caa gac aag agc 480
 Pro His Gly Gln Ala Leu Met Gly Gly Gln Arg Thr Gln Asp Lys Ser
 145 150 155 160

cag ggt gct aag cag acg ccc cta tgg gac atg ggc cag ccg atg ttt 528
 Gln Gly Ala Lys Gln Thr Pro Leu Trp Asp Met Gly Gln Pro Met Phe
 165 170 175

gga tgc ttc caa aca cca aca aca gtt ttg gac gag taa 567
 Gly Cys Phe Gln Thr Pro Thr Thr Val Leu Asp Glu *
 180 185

<210> 296

<211> 188

<212> PRT

<213> Homo sapiens

<400> 296

Met Ser Arg Asp His Arg Leu Leu Cys Leu Leu Gly Leu Cys Cys Val
 1 5 10 15
 Ala Asp Ala Ser Lys Gln Pro Phe Arg Lys Ser Gly Ile Pro Arg Gly
 20 25 30
 Tyr Thr Leu His Leu Arg Pro Ser Gly Tyr Asn Pro Asn Ser Gly Cys
 35 40 45
 Gly Trp Arg Gln Ser Tyr Tyr Thr Met Leu Pro Ser Lys Leu His Phe
 50 55 60
 Ile Trp Asn Arg Cys Gly Trp Gln Ala Glu Pro Leu Asn Thr Ala Ile
 65 70 75 80
 Gln Val Asn His Ala Asp Leu Leu Glu His Ala Gly Pro Arg Gly Gly
 85 90 95
 Pro His Tyr Arg Phe Pro His Ser Gly Asp Gly Glu Asn Leu Ile Cys
 100 105 110
 Leu Arg Ser Thr Ala Ser Val Cys Lys Gly Pro Ile Gln Val Gln Ile
 115 120 125

Gly Val Leu Thr Arg Thr Val Phe Gly Ala Ala Pro Leu Gln Thr Glu
 130 135 140
 Pro His Gly Gln Ala Leu Met Gly Gly Gln Arg Thr Gln Asp Lys Ser
 145 150 155 160
 Gln Gly Ala Lys Gln Thr Pro Leu Trp Asp Met Gly Gln Pro Met Phe
 165 170 175
 Gly Cys Phe Gln Thr Pro Thr Thr Val Leu Asp Glu
 180 185

<210> 297
 <211> 852
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(852)

<400> 297

atg gtt tcg gcg gca gcc ccc agc ctc ctc atc ctt ctg ttg ctg ctc	48
Met Val Ser Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu	
1 5 10 15	
ctg ggg tct gtg cct gct acc gac gcc cgc tct gtg ccc ctg aag gcc	96
Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu Lys Ala	
20 25 30	
acg ttc ctg gag gat gtg gcg ggt agt ggg gag gcc gag ggc tcg tcg	144
Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu Gly Ser Ser	
35 40 45	
gcc tcc tcc ccg agc ctc ccg cca ccc tgg acc ccg gcc ctc agc ccc	192
Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro Ala Leu Ser Pro	
50 55 60	
aca tcg atg ggg ccc cag ccc ata acc ctg ggg ggc cca tca ccc ccc	240
Thr Ser Met Gly Pro Gln Pro Ile Thr Leu Gly Gly Pro Ser Pro Pro	
65 70 75 80	
acc aac ttc ctg gat ggg ata gtg gac ttc ttc cgc cag tac gtg atg	288
Thr Asn Phe Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met	
85 90 95	

ctg	att	gct	gtg	gtg	ggc	tcc	ctg	gcc	ttt	ctg	ctg	atg	ttc	atc	gtc	336
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val	
		100						105					110			
tgt	gcc	gcg	gtc	atc	acc	cgg	cag	aag	cag	aag	gcc	tcg	gcc	tat	tac	384
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	
		115					120					125				
cca	tcg	tcc	ttc	ccc	aag	aag	aag	tac	gtg	gac	cag	agt	gac	cgg	gcc	432
Pro	Ser	Ser	Phe	Pro	Lys	Lys	Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	
		130					135					140				
ggg	ggc	ccc	cgg	gcc	ttc	agt	gag	gtc	ccc	gac	aga	gcc	ccc	gac	agc	480
Gly	Gly	Pro	Arg	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	
145					150					155					160	
agg	ccc	gag	gaa	gcc	ctg	gat	tcc	tcc	cgg	cag	ctc	cag	gcc	gac	atc	528
Arg	Pro	Glu	Glu	Ala	Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	
				165					170						175	
ttg	gcc	gcc	acc	cag	aac	ctc	aag	tcc	ccc	acc	agg	gct	gca	ctg	ggc	576
Leu	Ala	Ala	Thr	Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	
			180					185					190			
ggt	ggg	gac	gga	gcc	agg	atg	gtg	gag	ggc	agg	ggc	gca	gag	gaa	gag	624
Gly	Gly	Asp	Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	
		195					200					205				
gag	aag	ggc	agc	cag	gag	ggg	gac	cag	gaa	gtc	cag	gga	cat	ggg	gtc	672
Glu	Lys	Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	
	210					215					220					
cca	gtg	gag	aca	cca	gag	gcg	cag	gag	gag	ccg	tgc	tca	ggg	gtc	ctt	720
Pro	Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
225					230					235					240	
gag	ggg	gct	gtg	gtg	gcc	ggt	gag	ggc	caa	ggg	gag	ctg	gaa	ggg	tct	768
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	Ser	
				245					250					255		
ctc	ttg	tta	gcc	cag	gaa	gcc	cag	gga	cca	gtg	ggt	ccc	ccc	gaa	agc	816
Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	Glu	Ser	
			260					265					270			

852

<400> 298

Met 1	Val	Ser	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	Leu	15
Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	Lys	Ala
			20					25					30		
Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser
		35					40						45		
Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	Ala	Leu	Ser	Pro
	50					55					60				
Thr	Ser	Met	Gly	Pro	Gln	Pro	Ile	Thr	Leu	Gly	Gly	Pro	Ser	Pro	Pro
65				70						75					80
Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met
			85					90						95	
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val
			100					105					110		
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr
		115					120					125			
Pro	Ser	Ser	Phe	Pro	Lys	Lys	Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala
	130					135					140				
Gly	Gly	Pro	Arg	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser
145				150						155					160
Arg	Pro	Glu	Glu	Ala	Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile
			165						170					175	
Leu	Ala	Ala	Thr	Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly
			180					185					190		
Gly	Gly	Asp	Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu
		195					200					205			
Glu	Lys	Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val
	210					215					220				
Pro	Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
225				230						235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	Ser

245 250 255
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270
 Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
 275 280

<210> 299
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(369)

<400> 299
 atg gcc ctg ggc aag gtt ctg gcc atg gca ctg gtt ttg gcc ttg gcc 48
 Met Ala Leu Gly Lys Val Leu Ala Met Ala Leu Val Leu Ala Leu Ala
 1 5 10 15
 gtg ctg ggg tcg ctg tcc cct ggg gcc cgg gcg ggg gac tgc aag ggg 96
 Val Leu Gly Ser Leu Ser Pro Gly Ala Arg Ala Gly Asp Cys Lys Gly
 20 25 30
 cag cgg cag gtg ctg cgg gag gcg cca ggc ttc gtg acg gat ggt gcg 144
 Gln Arg Gln Val Leu Arg Glu Ala Pro Gly Phe Val Thr Asp Gly Ala
 35 40 45
 ggc aac tac agc gtc aat ggc aac tgc gag tgg ctc atc gag gaa ccc 192
 Gly Asn Tyr Ser Val Asn Gly Asn Cys Glu Trp Leu Ile Glu Glu Pro
 50 55 60
 tgc ccc agt ggc tct ttc tct gtg aag aca tgt ggc tta acc tgg ggt 240
 Cys Pro Ser Gly Ser Phe Ser Val Lys Thr Cys Gly Leu Thr Trp Gly
 65 70 75 80
 ata gct gag atc aga ggc atc tgt acg agg gag cag aag ggc att cca 288
 Ile Ala Glu Ile Arg Gly Ile Cys Thr Arg Glu Gln Lys Gly Ile Pro
 85 90 95
 ggc aag aat agc tgt gca aag gcg ggg aag cgg gag agt gat gct ttt 336
 Gly Lys Asn Ser Cys Ala Lys Ala Gly Lys Arg Glu Ser Asp Ala Phe
 100 105 110

gaa gaa cta gaa atc cag tgt gtt aaa aca tag
 Glu Glu Leu Glu Ile Gln Cys Val Lys Thr *
 115 120

369

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 300
 Met Ala Leu Gly Lys Val Leu Ala Met Ala Leu Val Leu Ala Leu Ala
 1 5 10 15
 Val Leu Gly Ser Leu Ser Pro Gly Ala Arg Ala Gly Asp Cys Lys Gly
 20 25 30
 Gln Arg Gln Val Leu Arg Glu Ala Pro Gly Phe Val Thr Asp Gly Ala
 35 40 45
 Gly Asn Tyr Ser Val Asn Gly Asn Cys Glu Trp Leu Ile Glu Glu Pro
 50 55 60
 Cys Pro Ser Gly Ser Phe Ser Val Lys Thr Cys Gly Leu Thr Trp Gly
 65 70 75 80
 Ile Ala Glu Ile Arg Gly Ile Cys Thr Arg Glu Gln Lys Gly Ile Pro
 85 90 95
 Gly Lys Asn Ser Cys Ala Lys Ala Gly Lys Arg Glu Ser Asp Ala Phe
 100 105 110
 Glu Glu Leu Glu Ile Gln Cys Val Lys Thr
 115 120

<210> 301
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(411)

<400> 301
 atg gac gca tac agc gcg tct tta agc ggt ccc aac agc ctc ggg ctg
 Met Asp Ala Tyr Ser Ala Ser Leu Ser Gly Pro Asn Ser Leu Gly Leu
 1 5 10 15

48

<400> 302
Met Asp Ala Tyr Ser Ala Ser Leu Ser Gly Pro Asn Ser Leu Gly Leu
1 5 10 15
Ser Thr Leu Val Pro Pro Ser Asn Ala Arg Glu Cys Pro Thr Glu Pro
20 25 30

Pro Lys Ile Leu Ser Leu Ser Val Pro Pro Ser Pro Ala Val Glu Pro
 35 40 45
 Arg Pro Arg Trp Lys Glu Asn Lys Thr Lys Ser Gly Ser Arg Gly Ser
 50 55 60
 Ser Ser Ala Asp Asn Cys Gln Gly Ser Asn Glu Leu Asn Gly Phe Pro
 65 70 75 80
 Glu Ala Ala Ile Thr Lys Thr Thr Lys Leu Val Ser Gln Gln Met Tyr
 85 90 95
 Ile Glu Cys Leu Leu His Thr Arg His Cys Cys Arg Pro Arg Glu Tyr
 100 105 110
 Ser Cys Glu Gln Asn Ser Glu Asp Thr Ser Ser Glu Thr Val Cys Gly
 115 120 125
 Asp Glu Asn Ala Pro Gln Glu Leu
 130 135

<210> 303

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(915)

<400> 303

atg ctg ccg ccg ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc	48
Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu	
1 5 10 15	
ctg cta ctg ctg gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca	96
Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro	
20 25 30	
tcc cca ggc cca gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg	144
Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala	
35 40 45	
gag ggc gag ggc tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg	192
Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro	
50 55 60	
cgg ggc tgc ctg gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg	240
Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp	

65	70	75	80	
gaa tgc gcc aac ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct				288
Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala				
	85	90	95	
cac ttc tac ggg cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca				336
His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr				
	100	105	110	
ggc ggc gac ctg agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt				384
Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys				
	115	120	125	
cgt tcg cag agt ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag				432
Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln				
	130	135	140	
atc tgc cgc ctg cag gag gcg gcc cgc gct ccg ccc gat gcc aac ctc				480
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu				
	145	150	155	160
act gtg gca cac ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca				528
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser				
	165	170	175	
cat cca tat gac act tgg aat gtg aca ggg cag gat gtg atc ttt ggc				576
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly				
	180	185	190	
tgt gaa gtg ttt gcc tac ccc atg gcc tcc atc gag tgg agg aag gat				624
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp				
	195	200	205	
ggc ttg gac atc cag ctg cca ggg gat gac ccc cac atc tct gtg cag				672
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln				
	210	215	220	
ttt agg ggt gga ccc cag agg ttt gag gtg act ggc tgg ctg cag atc				720
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile				
	225	230	235	240
cag gct gtg cgt ccc agt gat gag ggc act tac cgc tgc ctt ggc cgc				768

Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Arg
 245 250 255

aat gcc ctg ggt caa gtg gag gcc cct gct agc ttg aca gtg ctc aca 816
 Asn Ala Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr
 260 265 270

cct gac cag ctg aac tct aca ggc atc ccc cag ctg cga tca cta aac 864
 Pro Asp Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn
 275 280 285

ctg gtt cct gag gag gag gct gag agt gaa gag aat gac gat tac tac 912
 Leu Val Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
 290 295 300

tag 915
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<210> 304

<211> 304

<212> PRT

<213> Homo sapiens

<400> 304

Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
 1 5 10 15
 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
 20 25 30
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
 35 40 45
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
 50 55 60
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
 65 70 75 80
 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
 85 90 95
 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 100 105 110
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 115 120 125
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln

105230 " 226360

130 135 140
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 145 150 155 160
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 165 170 175
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 180 185 190
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 195 200 205
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 210 215 220
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 225 230 235 240
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Arg
 245 250 255
 Asn Ala Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr
 260 265 270
 Pro Asp Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn
 275 280 285
 Leu Val Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
 290 295 300

<210> 305

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(645)

<400> 305

atg ctg aat gtc tcc ggc ctc ttt gtt ctc ctc tgt ggg ctg ctt gtc 48
 Met Leu Asn Val Ser Gly Leu Phe Val Leu Leu Cys Gly Leu Leu Val
 1 5 10 15

tca tcc tct gca cag gag gtc ctg gct gga gtt tct tcc cag ctc ctt 96
 Ser Ser Ser Ala Gln Glu Val Leu Ala Gly Val Ser Ser Gln Leu Leu
 20 25 30

aat gat ttg act caa gga ctc ctc agg gca gac ttt ctt ccc agc ctg 144
 Asn Asp Leu Thr Gln Gly Leu Leu Arg Ala Asp Phe Leu Pro Ser Leu
 35 40 45

T00300"EE6360

cag aca act ggc ctc cag aaa cca ttg agt agt gcc ttc gat ggt gta Gln Thr Thr Gly Leu Gln Lys Pro Leu Ser Ser Ala Phe Asp Gly Val 50 55 60	192
tca ggc ctc ctg gac atc ttt gga cct cca ctc acc aat gag atc aac Ser Gly Leu Leu Asp Ile Phe Gly Pro Pro Leu Thr Asn Glu Ile Asn 65 70 75 80	240
act gtt agc ata cag gtg aaa aat cct caa ctc ctc cat gtc tcc atc Thr Val Ser Ile Gln Val Lys Asn Pro Gln Leu Leu His Val Ser Ile 85 90 95	288
gag agc acc cct caa aga aag gag gcc act gta caa gta cca ttc acg Glu Ser Thr Pro Gln Arg Lys Glu Ala Thr Val Gln Val Pro Phe Thr 100 105 110	336
tct gag ttg att gtg cag ctc ctg acc atg aag ccc ttc aca gct aat Ser Glu Leu Ile Val Gln Leu Leu Thr Met Lys Pro Phe Thr Ala Asn 115 120 125	384
atg cag tca gat ata aaa gtc cag att cgt ttg gag aag aat gta ggt Met Gln Ser Asp Ile Lys Val Gln Ile Arg Leu Glu Lys Asn Val Gly 130 135 140	432
ggc aga tat gag ctt gcc ttt ggg aac tgc agg ctc ttg ccc gag gct Gly Arg Tyr Glu Leu Ala Phe Gly Asn Cys Arg Leu Leu Pro Glu Ala 145 150 155 160	480
att tgg atc caa act gga gtc cat gag aaa aca caa ggt gca ata agc Ile Trp Ile Gln Thr Gly Val His Glu Lys Thr Gln Gly Ala Ile Ser 165 170 175	528
att aga cga gcc ata ccg cgg atc gta caa ccc acc gta tcc cat caa Ile Arg Arg Ala Ile Pro Arg Ile Val Gln Pro Thr Val Ser His Gln 180 185 190	576
cag cgc cta ggg ggc cga gct cga cag cat tct gcg cag cgt aaa ttc Gln Arg Leu Gly Gly Arg Ala Arg Gln His Ser Ala Gln Arg Lys Phe 195 200 205	624
gac gcc gac tcc ccc gtt tga Asp Ala Asp Ser Pro Val *	645

210

<210> 306
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 306

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Met Leu Asn Val Ser Gly Leu Phe Val Leu Leu Cys Gly Leu Leu Val
 1          5          10          15
Ser Ser Ser Ala Gln Glu Val Leu Ala Gly Val Ser Ser Gln Leu Leu
 20          25          30
Asn Asp Leu Thr Gln Gly Leu Leu Arg Ala Asp Phe Leu Pro Ser Leu
 35          40          45
Gln Thr Thr Gly Leu Gln Lys Pro Leu Ser Ser Ala Phe Asp Gly Val
 50          55          60
Ser Gly Leu Leu Asp Ile Phe Gly Pro Pro Leu Thr Asn Glu Ile Asn
65          70          75          80
Thr Val Ser Ile Gln Val Lys Asn Pro Gln Leu Leu His Val Ser Ile
 85          90          95
Glu Ser Thr Pro Gln Arg Lys Glu Ala Thr Val Gln Val Pro Phe Thr
100          105          110
Ser Glu Leu Ile Val Gln Leu Leu Thr Met Lys Pro Phe Thr Ala Asn
115          120          125
Met Gln Ser Asp Ile Lys Val Gln Ile Arg Leu Glu Lys Asn Val Gly
130          135          140
Gly Arg Tyr Glu Leu Ala Phe Gly Asn Cys Arg Leu Leu Pro Glu Ala
145          150          155          160
Ile Trp Ile Gln Thr Gly Val His Glu Lys Thr Gln Gly Ala Ile Ser
165          170          175
Ile Arg Arg Ala Ile Pro Arg Ile Val Gln Pro Thr Val Ser His Gln
180          185          190
Gln Arg Leu Gly Gly Arg Ala Arg Gln His Ser Ala Gln Arg Lys Phe
195          200          205
Asp Ala Asp Ser Pro Val
210

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<210> 307
 <211> 480
 <212> DNA
 <213> Homo sapiens

<221> CDS

<222> (1)...(480)

atg	agc	caa	gtg	tta	gcg	agc	ctt	gct	ctg	agc	agt	cgt	acg	gca	cag	48
Met	Ser	Gln	Val	Leu	Ala	Ser	Leu	Ala	Leu	Ser	Ser	Arg	Thr	Ala	Gln	
1				5					10					15		
gcg	cga	aca	ttg	aac	ctg	acg	aag	agc	aga	ttt	aaa	gga	ctc	gcc	gtc	96
Ala	Arg	Thr	Leu	Asn	Leu	Thr	Lys	Ser	Arg	Phe	Lys	Gly	Leu	Ala	Val	
			20					25					30			
cct	tgg	atg	gag	aaa	acc	act	gtt	gca	cag	gta	aga	acg	gca	tat	agc	144
Pro	Trp	Met	Glu	Lys	Thr	Thr	Val	Ala	Gln	Val	Arg	Thr	Ala	Tyr	Ser	
		35					40					45				
tgg	cac	gtg	cac	tac	cac	agc	ctc	tgc	ctc	gag	tgg	cca	tgg	cag	aca	192
Trp	His	Val	His	Tyr	His	Ser	Leu	Cys	Leu	Glu	Trp	Pro	Trp	Gln	Thr	
	50					55					60					
ctg	cca	ttc	aat	cct	ggt	ctg	aac	aca	acc	ccc	ttc	cca	aca	cag	ctg	240
Leu	Pro	Phe	Asn	Pro	Gly	Leu	Asn	Thr	Thr	Pro	Phe	Pro	Thr	Gln	Leu	
65					70					75					80	
tct	aca	tcc	tac	ccg	tca	gag	cag	gca	cac	cat	gtg	aaa	ctt	ctc	tgc	288
Ser	Thr	Ser	Tyr	Pro	Ser	Glu	Gln	Ala	His	His	Val	Lys	Leu	Leu	Cys	
				85					90					95		
cat	tcc	ttg	cct	agt	ggc	tct	gta	cac	agt	ggt	cct	aag	ctc	ctc	tat	336
His	Ser	Leu	Pro	Ser	Gly	Ser	Val	His	Ser	Val	Pro	Lys	Leu	Leu	Tyr	
			100					105					110			
tgg	gct	ccc	acg	gga	ctc	tat	att	cga	gac	cac	att	cca	cct	gcc	cta	384
Trp	Ala	Pro	Thr	Gly	Leu	Tyr	Ile	Arg	Asp	His	Ile	Pro	Pro	Ala	Leu	
		115					120					125				
atc	acc	ccg	ggg	cct	agt	acc	cgg	caa	cta	gga	aca	gcc	cca	gca	ccc	432
Ile	Thr	Pro	Gly	Pro	Ser	Thr	Arg	Gln	Leu	Gly	Thr	Ala	Pro	Ala	Pro	
	130					135					140					
ctg	aac	ccacta	caa	tta	ttc	aaa	cta	gcc	agt	gct	aaa	cct	gct	taa		480
Leu	Asn	Pro	Leu	Gln	Leu	Phe	Lys	Leu	Ala	Ser	Ala	Lys	Pro	Ala	*	

155

<400> 308															
Met	Ser	Gln	Val	Leu	Ala	Ser	Leu	Ala	Leu	Ser	Ser	Arg	Thr	Ala	Gln
1				5					10					15	
Ala	Arg	Thr	Leu	Asn	Leu	Thr	Lys	Ser	Arg	Phe	Lys	Gly	Leu	Ala	Val
			20					25					30		
Pro	Trp	Met	Glu	Lys	Thr	Thr	Val	Ala	Gln	Val	Arg	Thr	Ala	Tyr	Ser
		35					40					45			
Trp	His	Val	His	Tyr	His	Ser	Leu	Cys	Leu	Glu	Trp	Pro	Trp	Gln	Thr
50						55					60				
Leu	Pro	Phe	Asn	Pro	Gly	Leu	Asn	Thr	Thr	Pro	Phe	Pro	Thr	Gln	Leu
65				70						75				80	
Ser	Thr	Ser	Tyr	Pro	Ser	Glu	Gln	Ala	His	His	Val	Lys	Leu	Leu	Cys
			85						90					95	
His	Ser	Leu	Pro	Ser	Gly	Ser	Val	His	Ser	Val	Pro	Lys	Leu	Leu	Tyr
			100					105					110		
Trp	Ala	Pro	Thr	Gly	Leu	Tyr	Ile	Arg	Asp	His	Ile	Pro	Pro	Ala	Leu
		115					120					125			
Ile	Thr	Pro	Gly	Pro	Ser	Thr	Arg	Gln	Leu	Gly	Thr	Ala	Pro	Ala	Pro
		130				135					140				
Leu	Asn	Pro	Leu	Gln	Leu	Phe	Lys	Leu	Ala	Ser	Ala	Lys	Pro	Ala	
145					150					155					

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<220>  
<221> CDS  
<222> (1)...(907)
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48

gcc ctt gca cct ggg acc cct gcc cgg aac ctc cct gag aat cac att	96
Ala Leu Ala Pro Gly Thr Pro Ala Arg Asn Leu Pro Glu Asn His Ile	
20 25 30	
gac ctc cca ggc cca gcg ctg tgg acg cct cag gcc agc cac cac cgc	144
Asp Leu Pro Gly Pro Ala Leu Trp Thr Pro Gln Ala Ser His His Arg	
35 40 45	
cgg cgg ggc ccg ggc aag aag gag tgg ggc cca ggc ctg ccc agc cag	192
Arg Arg Gly Pro Gly Lys Lys Glu Trp Gly Pro Gly Leu Pro Ser Gln	
50 55 60	
gcc cag gat ggg gct gtg gtc acc gcc acc agg cag gcc tcc agg ctg	240
Ala Gln Asp Gly Ala Val Val Thr Ala Thr Arg Gln Ala Ser Arg Leu	
65 70 75 80	
cca gag gct gag ggg ctg ctg cct gag cag agt cct gca ggc ctg ctg	288
Pro Glu Ala Glu Gly Leu Leu Pro Glu Gln Ser Pro Ala Gly Leu Leu	
85 90 95	
cag gac aag gac ctg ctc ctg gga ctg gca ttg ccc tac ccc gag aag	336
Gln Asp Lys Asp Leu Leu Leu Gly Leu Ala Leu Pro Tyr Pro Glu Lys	
100 105 110	
gag aac cga cct cca ggt tgg gag agg acc agg aaa cgc agc agg gag	384
Glu Asn Arg Pro Pro Gly Trp Glu Arg Thr Arg Lys Arg Ser Arg Glu	
115 120 125	
cac aag aga cgc agg gac agg ttg agg ctg cac caa ggc cga gcc ttg	432
His Lys Arg Arg Arg Asp Arg Leu Arg Leu His Gln Gly Arg Ala Leu	
130 135 140	
gtc cga ggt ccc agc tcc ctg atg aag aag gca gag ctc tcc gaa gcc	480
Val Arg Gly Pro Ser Ser Leu Met Lys Lys Ala Glu Leu Ser Glu Ala	
145 150 155 160	
cag gtg ctg gat gca gcc atg gag gaa tcc tcc acc agc ctg gcg ccc	528
Gln Val Leu Asp Ala Ala Met Glu Glu Ser Ser Thr Ser Leu Ala Pro	
165 170 175	
acc atg ttc ttt ctc acc acc ttt gag gca gca cct gcc aca gaa gag	576
Thr Met Phe Phe Leu Thr Thr Phe Glu Ala Ala Pro Ala Thr Glu Glu	

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<210> 310
<211> 302
<212> PRT
<213> Homo sapiens
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<400> 310															
Met	Leu	Phe	Leu	Val	Leu	Leu	Leu	Pro	Leu	Glu	Leu	Ser	Leu	Ala	Gly
1				5					10					15	
Ala	Leu	Ala	Pro	Gly	Thr	Pro	Ala	Arg	Asn	Leu	Pro	Glu	Asn	His	Ile
			20					25					30		
Asp	Leu	Pro	Gly	Pro	Ala	Leu	Trp	Thr	Pro	Gln	Ala	Ser	His	His	Arg
		35					40					45			

Arg Arg Gly Pro Gly Lys Lys Glu Trp Gly Pro Gly Leu Pro Ser Gln
 50 55 60
 Ala Gln Asp Gly Ala Val Val Thr Ala Thr Arg Gln Ala Ser Arg Leu
 65 70 75 80
 Pro Glu Ala Glu Gly Leu Leu Pro Glu Gln Ser Pro Ala Gly Leu Leu
 85 90 95
 Gln Asp Lys Asp Leu Leu Leu Gly Leu Ala Leu Pro Tyr Pro Glu Lys
 100 105 110
 Glu Asn Arg Pro Pro Gly Trp Glu Arg Thr Arg Lys Arg Ser Arg Glu
 115 120 125
 His Lys Arg Arg Arg Asp Arg Leu Arg Leu His Gln Gly Arg Ala Leu
 130 135 140
 Val Arg Gly Pro Ser Ser Leu Met Lys Lys Ala Glu Leu Ser Glu Ala
 145 150 155 160
 Gln Val Leu Asp Ala Ala Met Glu Glu Ser Ser Thr Ser Leu Ala Pro
 165 170 175
 Thr Met Phe Phe Leu Thr Thr Phe Glu Ala Ala Pro Ala Thr Glu Glu
 180 185 190
 Ser Leu Ile Leu Pro Val Thr Ser Leu Arg Pro Gln Gln Ala Gln Pro
 195 200 205
 Arg Ser Asp Gly Glu Val Met Pro Thr Leu Asp Met Ala Leu Phe Asp
 210 215 220
 Trp Thr Asp Tyr Glu Asp Leu Lys Pro Asp Gly Trp Pro Ser Ala Lys
 225 230 235 240
 Lys Lys Glu Lys His Arg Gly Lys Leu Ser Ser Asp Gly Asn Glu Thr
 245 250 255
 Ser Pro Ala Glu Gly Glu Pro Cys Asp His His Gln Asp Cys Leu Pro
 260 265 270
 Gly Thr Cys Cys Asp Leu Arg Glu His Leu Cys Thr Pro His Asn Arg
 275 280 285
 Gly Leu Asn Asn Lys Cys Phe Asp Asp Cys Met Cys Val Glu
 290 295 300

<210> 311

<211> 670

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(670)

<400> 311

atg gga atg gtt tac agt agt gcc ctt tta tcc ctg gtt ttg gtt gcc	48
Met Gly Met Val Tyr Ser Ser Ala Leu Leu Ser Leu Val Leu Val Ala	
1 5 10 15	
atg gtt tta gtt acc cac agt caa cca tgg tct gaa aac agg ggc caa	96
Met Val Leu Val Thr His Ser Gln Pro Trp Ser Glu Asn Arg Gly Gln	
20 25 30	
gct gct gca tcc tta tgt tct cag cca gag aaa cag cct agc aaa cgc	144
Ala Ala Ala Ser Leu Cys Ser Gln Pro Glu Lys Gln Pro Ser Lys Arg	
35 40 45	
atc caa tgt ggc ctt tcc tct gaa ttg gat acc ctg cca cac gtc tgc	192
Ile Gln Cys Gly Leu Ser Ser Glu Leu Asp Thr Leu Pro His Val Cys	
50 55 60	
atg tct gta ccc ctg ctg ata gga gtt tca gga atc gga gct atc tat	240
Met Ser Val Pro Leu Leu Ile Gly Val Ser Gly Ile Gly Ala Ile Tyr	
65 70 75 80	
cag ttg aac tct tca ccg atg aca aca gta atg aca aga gca cct gga	288
Gln Leu Asn Ser Ser Pro Met Thr Thr Val Met Thr Arg Ala Pro Gly	
85 90 95	
agt cct gtt ctc caa gca ctg gac ttc att ttt tat gtg aac aaa atg	336
Ser Pro Val Leu Gln Ala Leu Asp Phe Ile Phe Tyr Val Asn Lys Met	
100 105 110	
aaa atg aat gtg gaa gaa atg tgg aaa ggg atg agc ggt acg tca ttc	384
Lys Met Asn Val Glu Glu Met Trp Lys Gly Met Ser Gly Thr Ser Phe	
115 120 125	
ttc gct ctt cca aga aaa aaa gat att ctt cca cga tgg ttg agg ggc	432
Phe Ala Leu Pro Arg Lys Lys Asp Ile Leu Pro Arg Trp Leu Arg Gly	
130 135 140	
aaa cag ttg gta aaa ttc cag aat acc aag tca caa agc aga gaa tcg	480
Lys Gln Leu Val Lys Phe Gln Asn Thr Lys Ser Gln Ser Arg Glu Ser	
145 150 155 160	
tgt tcc ctc cca aat tta cat gtt gaa gtc ata aac cct gta att ctt	528
Cys Ser Leu Pro Asn Leu His Val Glu Val Ile Asn Pro Val Ile Leu	
165 170 175	

aat gtg act gta ttt gga aac agg gcc ttt aaa gaa gta att aag tat 576
 Asn Val Thr Val Phe Gly Asn Arg Ala Phe Lys Glu Val Ile Lys Tyr
 180 185 190
 tac att cag tgt agg cat tca ata agt tca ggc tta gtg aag gtt gtc 624
 Tyr Ile Gln Cys Arg His Ser Ile Ser Ser Gly Leu Val Lys Val Val
 195 200 205
 act gaa atc cca tca gct cag cag gga gca agg agc ctc ttt gaa a 670
 Thr Glu Ile Pro Ser Ala Gln Gln Gly Ala Arg Ser Leu Phe Glu
 210 215 220

<210> 312
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 312
 Met Gly Met Val Tyr Ser Ser Ala Leu Leu Ser Leu Val Leu Val Ala
 1 5 10 15
 Met Val Leu Val Thr His Ser Gln Pro Trp Ser Glu Asn Arg Gly Gln
 20 25 30
 Ala Ala Ala Ser Leu Cys Ser Gln Pro Glu Lys Gln Pro Ser Lys Arg
 35 40 45
 Ile Gln Cys Gly Leu Ser Ser Glu Leu Asp Thr Leu Pro His Val Cys
 50 55 60
 Met Ser Val Pro Leu Leu Ile Gly Val Ser Gly Ile Gly Ala Ile Tyr
 65 70 75 80
 Gln Leu Asn Ser Ser Pro Met Thr Thr Val Met Thr Arg Ala Pro Gly
 85 90 95
 Ser Pro Val Leu Gln Ala Leu Asp Phe Ile Phe Tyr Val Asn Lys Met
 100 105 110
 Lys Met Asn Val Glu Glu Met Trp Lys Gly Met Ser Gly Thr Ser Phe
 115 120 125
 Phe Ala Leu Pro Arg Lys Lys Asp Ile Leu Pro Arg Trp Leu Arg Gly
 130 135 140
 Lys Gln Leu Val Lys Phe Gln Asn Thr Lys Ser Gln Ser Arg Glu Ser
 145 150 155 160
 Cys Ser Leu Pro Asn Leu His Val Glu Val Ile Asn Pro Val Ile Leu
 165 170 175
 Asn Val Thr Val Phe Gly Asn Arg Ala Phe Lys Glu Val Ile Lys Tyr

180 185 190
 Tyr Ile Gln Cys Arg His Ser Ile Ser Ser Gly Leu Val Lys Val Val
 195 200 205
 Thr Glu Ile Pro Ser Ala Gln Gln Gly Ala Arg Ser Leu Phe Glu
 210 215 220

<210> 313
 <211> 426
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(426)

<400> 313

atg gaa ggg gac ccc ggg ggg ttg ctg ctg ctg ctg ctg gct ggg gtg 48
 Met Glu Gly Asp Pro Gly Gly Leu Leu Leu Leu Leu Leu Ala Gly Val
 1 5 10 15

ggg gga tat cag ctg gga act aga agg aac ttc tcc cat gga gaa aag 96
 Gly Gly Tyr Gln Leu Gly Thr Arg Arg Asn Phe Ser His Gly Glu Lys
 20 25 30

gta aac gat aag atc cca gta gcc acc atc agc atc tgg gac aaa tac 144
 Val Asn Asp Lys Ile Pro Val Ala Thr Ile Ser Ile Trp Asp Lys Tyr
 35 40 45

agc cct cac cac tgg ggt ccc ctg cag tcc tca cag gca cta agc cca 192
 Ser Pro His His Trp Gly Pro Leu Gln Ser Ser Gln Ala Leu Ser Pro
 50 55 60

cct gag gga gct aac tgg agc cca cac agc tgt gct gtc tcc aca aaa 240
 Pro Glu Gly Ala Asn Trp Ser Pro His Ser Cys Ala Val Ser Thr Lys
 65 70 75 80

gga gct gat act gtg cac tgc cct cgg tgg tcc acg cag cta cta tac 288
 Gly Ala Asp Thr Val His Cys Pro Arg Trp Ser Thr Gln Leu Leu Tyr
 85 90 95

tgc acc atc cta gaa cta gga cta cca cta gag tgt gcc tta cta caa 336
 Cys Thr Ile Leu Glu Leu Gly Leu Pro Leu Glu Cys Ala Leu Leu Gln
 100 105 110

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

ggc gtc aga ctc cag gat ctt gga ctt ttg gaa tct tgg att tac acc 384
 Gly Val Arg Leu Gln Asp Leu Gly Leu Leu Glu Ser Trp Ile Tyr Thr
 115 120 125

agt ggt cta cct gag gct ctt ggg cct ccg gcc ata gag tga 426
 Ser Gly Leu Pro Glu Ala Leu Gly Pro Pro Ala Ile Glu *
 130 135 140

<210> 314
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 314
 Met Glu Gly Asp Pro Gly Gly Leu Leu Leu Leu Leu Ala Gly Val
 1 5 10 15
 Gly Gly Tyr Gln Leu Gly Thr Arg Arg Asn Phe Ser His Gly Glu Lys
 20 25 30
 Val Asn Asp Lys Ile Pro Val Ala Thr Ile Ser Ile Trp Asp Lys Tyr
 35 40 45
 Ser Pro His His Trp Gly Pro Leu Gln Ser Ser Gln Ala Leu Ser Pro
 50 55 60
 Pro Glu Gly Ala Asn Trp Ser Pro His Ser Cys Ala Val Ser Thr Lys
 65 70 75 80
 Gly Ala Asp Thr Val His Cys Pro Arg Trp Ser Thr Gln Leu Leu Tyr
 85 90 95
 Cys Thr Ile Leu Glu Leu Gly Leu Pro Leu Glu Cys Ala Leu Leu Gln
 100 105 110
 Gly Val Arg Leu Gln Asp Leu Gly Leu Leu Glu Ser Trp Ile Tyr Thr
 115 120 125
 Ser Gly Leu Pro Glu Ala Leu Gly Pro Pro Ala Ile Glu
 130 135 140

<210> 315
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(375)

<400> 315

atg	gtc	ctg	tgc	tgg	ctg	ctg	ctt	ctg	gtg	atg	gct	ctg	ccc	cca	ggc	48
Met	Val	Leu	Cys	Trp	Leu	Leu	Leu	Leu	Val	Met	Ala	Leu	Pro	Pro	Gly	
1				5					10					15		

acg	acg	ggc	gtc	aag	gac	tgc	gtc	ttc	tgt	gag	ctc	acc	gac	tcc	atg	96
Thr	Thr	Gly	Val	Lys	Asp	Cys	Val	Phe	Cys	Glu	Leu	Thr	Asp	Ser	Met	
		20						25					30			

cag	tgt	cct	ggt	acc	tac	atg	cac	tgt	ggc	gat	gac	gag	gac	tgc	ttc	144
Gln	Cys	Pro	Gly	Thr	Tyr	Met	His	Cys	Gly	Asp	Asp	Glu	Asp	Cys	Phe	
		35					40					45				

aca	ggc	cac	ggg	gtc	gcc	ccg	ggc	act	ggt	ccg	gtc	atc	aac	aaa	ggc	192
Thr	Gly	His	Gly	Val	Ala	Pro	Gly	Thr	Gly	Pro	Val	Ile	Asn	Lys	Gly	
	50					55				60						

tgc	ctg	cga	gcc	acc	agc	tgc	ggc	ctt	gag	gaa	ccc	gtc	agc	tac	agg	240
Cys	Leu	Arg	Ala	Thr	Ser	Cys	Gly	Leu	Glu	Glu	Pro	Val	Ser	Tyr	Arg	
65					70				75					80		

ggc	gtc	acc	tac	agc	ctc	acc	acc	aac	tgc	tgc	acc	ggc	cgc	ctg	tgt	288
Gly	Val	Thr	Tyr	Ser	Leu	Thr	Thr	Asn	Cys	Cys	Thr	Gly	Arg	Leu	Cys	
				85				90						95		

aac	aga	gcc	ccg	agc	agc	cag	aca	gtg	ggg	gcc	acc	acc	agc	ctg	gca	336
Asn	Arg	Ala	Pro	Ser	Ser	Gln	Thr	Val	Gly	Ala	Thr	Thr	Ser	Leu	Ala	
		100						105					110			

ctg	ggg	ctg	ggt	atg	ctg	ctt	cct	cca	cgt	ttg	ctg	tga				375
Leu	Gly	Leu	Gly	Met	Leu	Leu	Pro	Pro	Arg	Leu	Leu	*				
	115						120									

<210> 316

<211> 124

<212> PRT

<213> Homo sapiens

<400> 316

Met	Val	Leu	Cys	Trp	Leu	Leu	Leu	Leu	Val	Met	Ala	Leu	Pro	Pro	Gly	
1				5					10						15	

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<210> 317
<211> 688
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(688)

<400> 317
atg gag ccc ctg cgc gcg ccc gcg ctg cgc cgc ctg ctg ccg ccg ctg
Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
  1              5              10              15

ctg ctc ctg ctg ctg tca ctg ccc ccc cgc gcc cgg gcc aag tac gtg
Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
      20              25              30

cgg ggc aac ctc agt tcc aag gag gac tgg gtg ttc ctg aca aga ttt
Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
      35              40              45

tgt ttc ctc tcg gat tac ggc cga ctg gac ttc cgt ttc cgc tac cct
Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
      50              55              60

gag gcc aag tgc tgt cag aac atc ctc ctc tat ttt gat gac cca tcc
Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser

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<220>  
<221> CDS  
<222> (1)...(688)
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<400> 317

ctg ctc ctg ctg ctg tca ctg ccc ccc cgc gcc cgg gcc aag tac gtg 96
Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
20 25 30

cgg ggc aac ctc agt tcc aag gag gac tgg gtg ttc ctg aca aga ttt 144
Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
35 40 45

tgt ttc ctc tcg gat tac ggc cga ctg gac ttc cgt ttc cgc tac cct 192
Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
50 55 60

gag gcc aag tgc tgt cag aac atc ctc ctc tat ttt gat gac cca tcc 240
Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser

65	70	75	80	
cag tgg cca gcc gtg tac aag gca ggg gac aag gac tgc ctg gcc aag				288
Gln Trp Pro Ala Val Tyr Lys Ala Gly Asp Lys Asp Cys Leu Ala Lys				
	85	90	95	
gag tca gtg atc cgg ccg gag aac aac cag gtc atc aac ctc acc acc				336
Glu Ser Val Ile Arg Pro Glu Asn Asn Gln Val Ile Asn Leu Thr Thr				
	100	105	110	
cag tat gcc tgg tcc ggc tgt cag gtg gta tca gag gag gga acc cgc				384
Gln Tyr Ala Trp Ser Gly Cys Gln Val Val Ser Glu Glu Gly Thr Arg				
	115	120	125	
tac ctg agc tgc tcc agt ggc cgc agc ttc cgc tca gtg cgt gaa cgg				432
Tyr Leu Ser Cys Ser Ser Gly Arg Ser Phe Arg Ser Val Arg Glu Arg				
	130	135	140	
tgg tgg tat att gcg ctc agc aag tgt ggg ggt gat gga ttg cag ctg				480
Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu				
	145	150	155	160
gag tat gag atg gtc ctc acc aat ggc aag tcc ttc tgg aca cga cac				528
Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His				
	165	170	175	
ttc tcc gct gat gag ttt ggg atc ctg gag aca gat gtg acc ttc ctc				576
Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu				
	180	185	190	
ctc atc ttc atc ctc atc ttc ttc ctc tct tgt tac ttt gga tat ttg				624
Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu				
	195	200	205	
ctg aaa ggt cgt cag ttg ctc cac aca act tat aaa atg ttc atg gcc				672
Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala				
	210	215	220	
gca gca gga gta gag g				688
Ala Ala Gly Val Glu				
	225			

<210> 318
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 318

Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
 20 25 30
 Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
 35 40 45
 Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
 50 55 60
 Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser
 65 70 75 80
 Gln Trp Pro Ala Val Tyr Lys Ala Gly Asp Lys Asp Cys Leu Ala Lys
 85 90 95
 Glu Ser Val Ile Arg Pro Glu Asn Asn Gln Val Ile Asn Leu Thr Thr
 100 105 110
 Gln Tyr Ala Trp Ser Gly Cys Gln Val Val Ser Glu Glu Gly Thr Arg
 115 120 125
 Tyr Leu Ser Cys Ser Ser Gly Arg Ser Phe Arg Ser Val Arg Glu Arg
 130 135 140
 Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu
 145 150 155 160
 Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His
 165 170 175
 Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu
 180 185 190
 Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu
 195 200 205
 Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala
 210 215 220
 Ala Ala Gly Val Glu
 225

<210> 319
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(765)

<400> 319

atg gga gct cca aag ctg gcc aag ctg cac aca gcc ctg ctg gcg tcc	48
Met Gly Ala Pro Lys Leu Ala Lys Leu His Thr Ala Leu Leu Ala Ser	
1 5 10 15	

agc ctg gct cta ggc cag gag cct tgg ctg gag ggc ggc cca gcg ccc	96
Ser Leu Ala Leu Gly Gln Glu Pro Trp Leu Glu Gly Gly Pro Ala Pro	
20 25 30	

cga cag cca cgt cca gca cct tca gca ggt tct ccc cgg cag cac ttg	144
Arg Gln Pro Arg Pro Ala Pro Ser Ala Gly Ser Pro Arg Gln His Leu	
35 40 45	

gca gtc aga tgt ggc cag acg gtc cct tcc aga gag agc tgt cgt ggc	192
Ala Val Arg Cys Gly Gln Thr Val Pro Ser Arg Glu Ser Cys Arg Gly	
50 55 60	

ccc aaa ggc atg aac gtg gcc ctc cgt gca cgg caa gca gta cag gaa	240
Pro Lys Gly Met Asn Val Ala Leu Arg Ala Arg Gln Ala Val Gln Glu	
65 70 75 80	

cgt gtt cgg aag gca gag tgc gcg gcc aac agc tgt gct gcc ctg gac	288
Arg Val Arg Lys Ala Glu Cys Ala Ala Asn Ser Cys Ala Ala Leu Asp	
85 90 95	

aag tgc cct cca cct caa cag ttt ccc ctg caa ggc ctc cat gat gag	336
Lys Cys Pro Pro Pro Gln Gln Phe Pro Leu Gln Gly Leu His Asp Glu	
100 105 110	

cgg aac aca gcc act cct ggg gaa ggg cac aag cag cag tca cac gtc	384
Arg Asn Thr Ala Thr Pro Gly Glu Gly His Lys Gln Gln Ser His Val	
115 120 125	

gca ctg aag tgg ctg gat gga cgc cag aga gtc cag agg cag aca gga	432
Ala Leu Lys Trp Leu Asp Gly Arg Gln Arg Val Gln Arg Gln Thr Gly	
130 135 140	

aac aca aaa tgg aag atg ctg gtg cac gca gaa agt ctt gga gga gga	480
Asn Thr Lys Trp Lys Met Leu Val His Ala Glu Ser Leu Gly Gly Gly	
145 150 155 160	

gcc ctg tgg cat tgg cca caa atg agc aca tcc atc agc tcc tga 765
Ala Leu Trp His Trp Pro Gln Met Ser Thr Ser Ile Ser Ser *
245 250

<400> 320

Met	Gly	Ala	Pro	Lys	Leu	Ala	Lys	Leu	His	Thr	Ala	Leu	Leu	Ala	Ser
1				5				10						15	
Ser	Leu	Ala	Leu	Gly	Gln	Glu	Pro	Trp	Leu	Glu	Gly	Gly	Pro	Ala	Pro
			20					25					30		
Arg	Gln	Pro	Arg	Pro	Ala	Pro	Ser	Ala	Gly	Ser	Pro	Arg	Gln	His	Leu
		35					40					45			
Ala	Val	Arg	Cys	Gly	Gln	Thr	Val	Pro	Ser	Arg	Glu	Ser	Cys	Arg	Gly
	50					55					60				
Pro	Lys	Gly	Met	Asn	Val	Ala	Leu	Arg	Ala	Arg	Gln	Ala	Val	Gln	Glu
65				70						75				80	
Arg	Val	Arg	Lys	Ala	Glu	Cys	Ala	Ala	Asn	Ser	Cys	Ala	Ala	Leu	Asp

85 90 95
 Lys Cys Pro Pro Pro Gln Gln Phe Pro Leu Gln Gly Leu His Asp Glu
 100 105 110
 Arg Asn Thr Ala Thr Pro Gly Glu Gly His Lys Gln Gln Ser His Val
 115 120 125
 Ala Leu Lys Trp Leu Asp Gly Arg Gln Arg Val Gln Arg Gln Thr Gly
 130 135 140
 Asn Thr Lys Trp Lys Met Leu Val His Ala Glu Ser Leu Gly Gly Gly
 145 150 155 160
 Glu Pro Glu Thr Phe Thr Lys Ser Lys Ser Asp Leu Val Ser Ala His
 165 170 175
 Phe Thr Pro Ser Gln Leu Leu Thr Leu Pro Pro Ile Phe Thr Asp Lys
 180 185 190
 Glu Thr Glu Ser Gln Arg Pro Gly Asn Gly Glu Gly Gly Glu Ser Gly
 195 200 205
 Gln Val Ala Gly Thr Gly Leu Pro Leu Gly Gln Leu Met Asn Pro Gly
 210 215 220
 Ser Ser Ile Arg Asp Thr Gly Glu Pro Asn Thr Ser Cys His Cys Val
 225 230 235 240
 Ala Leu Trp His Trp Pro Gln Met Ser Thr Ser Ile Ser Ser
 245 250

<210> 321
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(339)

<400> 321
 atg gtg ctc acc aat acg gct tct ttc tat gca gct ctg cag cta ctg 48
 Met Val Leu Thr Asn Thr Ala Ser Phe Tyr Ala Ala Leu Gln Leu Leu
 1 5 10 15
 ctg gct ctt ctg gga att ttt tct ttt gta tat ccg tcc ctg gtg gat 96
 Leu Ala Leu Leu Gly Ile Phe Ser Phe Val Tyr Pro Ser Leu Val Asp
 20 25 30
 cac ttg ccc ttt cct gcc aaa ccc ttg cct ctg tct gaa ttc tgg ttt 144
 His Leu Pro Phe Pro Ala Lys Pro Leu Pro Leu Ser Glu Phe Trp Phe
 35 40 45

ggc tct tcc ttt gtg gcc ccc aga gcc tct gcc aat ctt gtt gga gca 192
 Gly Ser Ser Phe Val Ala Pro Arg Ala Ser Ala Asn Leu Val Gly Ala
 50 55 60

ttt gca gca ata gga aaa agg tcc ccc ttc ttc agg gca ccc atg atc 240
 Phe Ala Ala Ile Gly Lys Arg Ser Pro Phe Phe Arg Ala Pro Met Ile
 65 70 75 80

ttg aaa cag aga ctc atg aag act cat gaa tgg gtt tca act ccc atc 288
 Leu Lys Gln Arg Leu Met Lys Thr His Glu Trp Val Ser Thr Pro Ile
 85 90 95

cat cct ctc tgc caa gcc ctt gtg gag acc aca gtc cat gac cct gaa 336
 His Pro Leu Cys Gln Ala Leu Val Glu Thr Thr Val His Asp Pro Glu
 100 105 110

taa 339
 *

<210> 322

<211> 112

<212> PRT

<213> Homo sapiens

<400> 322

Met Val Leu Thr Asn Thr Ala Ser Phe Tyr Ala Ala Leu Gln Leu Leu
 1 5 10 15
 Leu Ala Leu Leu Gly Ile Phe Ser Phe Val Tyr Pro Ser Leu Val Asp
 20 25 30
 His Leu Pro Phe Pro Ala Lys Pro Leu Pro Leu Ser Glu Phe Trp Phe
 35 40 45
 Gly Ser Ser Phe Val Ala Pro Arg Ala Ser Ala Asn Leu Val Gly Ala
 50 55 60
 Phe Ala Ala Ile Gly Lys Arg Ser Pro Phe Phe Arg Ala Pro Met Ile
 65 70 75 80
 Leu Lys Gln Arg Leu Met Lys Thr His Glu Trp Val Ser Thr Pro Ile
 85 90 95
 His Pro Leu Cys Gln Ala Leu Val Glu Thr Thr Val His Asp Pro Glu
 100 105 110

T083930" 4446860

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<220>
<221> CDS
<222> (1)...(888)
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atg	cgc	ctc	cac	ctg	ctc	ctg	ctg	ctc	gcg	ctg	tgc	ggt	gca	ggc	acc	48
Met	Arg	Leu	His	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Cys	Gly	Ala	Gly	Thr	
1				5					10					15		
acc	gcc	gcg	gag	ctc	agt	tac	agc	ttg	cgt	ggc	aac	tgg	agc	atc	tgc	96
Thr	Ala	Ala	Glu	Leu	Ser	Tyr	Ser	Leu	Arg	Gly	Asn	Trp	Ser	Ile	Cys	
			20					25					30			
aat	ggg	aac	ggc	tcg	ctg	gag	ctg	ccc	ggg	gcg	gtc	cct	ggc	tgc	gtg	144
Asn	Gly	Asn	Gly	Ser	Leu	Glu	Leu	Pro	Gly	Ala	Val	Pro	Gly	Cys	Val	
		35					40					45				
cac	agc	gcc	ttg	ttc	cag	cag	ggc	ctg	atc	cag	gtc	act	ctg	ttg	tgt	192
His	Ser	Ala	Leu	Phe	Gln	Gln	Gly	Leu	Ile	Gln	Val	Thr	Leu	Leu	Cys	
	50					55				60						
gaa	ggc	tac	agt	gca	gga	gag	tgg	aag	cct	gga	gac	caa	cca	ggg	gac	240
Glu	Gly	Tyr	Ser	Ala	Gly	Glu	Trp	Lys	Pro	Gly	Asp	Gln	Pro	Gly	Asp	
65					70				75					80		
tat	tgc	tgg	tct	atg	tat	ggg	caa	gag	atg	act	tct	ggc	ttg	gac	aag	288
Tyr	Cys	Trp	Ser	Met	Tyr	Gly	Gln	Glu	Met	Thr	Ser	Gly	Leu	Asp	Lys	
				85				90					95			
cat	ggt	ggc	agt	gaa	atg	ctc	caa	aca	cat	ttc	tac	acc	gat	aac	aag	336
His	Gly	Gly	Ser	Glu	Met	Leu	Gln	Thr	His	Phe	Tyr	Thr	Asp	Asn	Lys	
			100					105					110			
aaa	tat	gct	gta	aat	gat	gtt	tcc	ttc	tca	atc	cct	gcc	gcc	tct	gaa	384
Lys	Tyr	Ala	Val	Asn	Asp	Val	Ser	Phe	Ser	Ile	Pro	Ala	Ala	Ser	Glu	
		115					120					125				
ttt	gct	gac	ctt	agt	aac	atc	atc	aat	aaa	tta	cta	aag	gac	aaa	aat	432

Phe	Ala	Asp	Leu	Ser	Asn	Ile	Ile	Asn	Lys	Leu	Leu	Lys	Asp	Lys	Asn		
130						135				140							
gag ttc cac aaa cat atg gag ttt tat ttc ctt att aag ggc cag ttt 480																	
Glu	Phe	His	Lys	His	Met	Glu	Phe	Tyr	Phe	Leu	Ile	Lys	Gly	Gln	Phe		
145					150					155					160		
ctg cga atg tcc ttg gtc aaa cac atg gaa ctg gag aac atg tca tca 528																	
Leu	Arg	Met	Ser	Leu	Val	Lys	His	Met	Glu	Leu	Glu	Asn	Met	Ser	Ser		
				165					170					175			
gaa gta gtt gtg gaa ata gaa tat gtg aag tac aca gca ccc cag cca 576																	
Glu	Val	Val	Val	Glu	Ile	Glu	Tyr	Val	Lys	Tyr	Thr	Ala	Pro	Gln	Pro		
			180					185					190				
gag caa tgc atg ttc cat gat gac tgg atc ctt tca gtt aaa ggg gca 624																	
Glu	Gln	Cys	Met	Phe	His	Asp	Asp	Trp	Ile	Leu	Ser	Val	Lys	Gly	Ala		
		195					200					205					
aag gaa tgg atc ttg act ggt tct tat gat aag acc tct caa atc cgg 672																	
Lys	Glu	Trp	Ile	Leu	Thr	Gly	Ser	Tyr	Asp	Lys	Thr	Ser	Gln	Ile	Arg		
	210					215				220							
tcc ttg gaa aga aag tca ata atg aca att gtt gga cat agg gat gtc 720																	
Ser	Leu	Glu	Arg	Lys	Ser	Ile	Met	Thr	Ile	Val	Gly	His	Arg	Asp	Val		
225					230					235					240		
tta aaa gat gtg gcc tgg gcc aaa aaa aaa gat agt ttg tct tgc tta 768																	
Leu	Lys	Asp	Val	Ala	Trp	Ala	Lys	Lys	Lys	Asp	Ser	Leu	Ser	Cys	Leu		
			245					250						255			
ttt gtg agt gcc tct atg gat cca act att ctc tta tgg gag tgg aat 816																	
Phe	Val	Ser	Ala	Ser	Met	Asp	Pro	Thr	Ile	Leu	Leu	Trp	Glu	Trp	Asn		
			260					265					270				
aga gag aaa caa agt gaa agc ccg acc gtg ctg cag agg tca tgc tgg 864																	
Arg	Glu	Lys	Gln	Ser	Glu	Ser	Pro	Thr	Val	Leu	Gln	Arg	Ser	Cys	Trp		
		275					280					285					
aag tgc aga gtc tat agc tgt tga 888																	
Lys	Cys	Arg	Val	Tyr	Ser	Cys	*										
	290					295											

<210> 324
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 324

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Met Arg Leu His Leu Leu Leu Leu Leu Ala Leu Cys Gly Ala Gly Thr
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Thr Ala Ala Glu Leu Ser Tyr Ser Leu Arg Gly Asn Trp Ser Ile Cys
 20          25          30
Asn Gly Asn Gly Ser Leu Glu Leu Pro Gly Ala Val Pro Gly Cys Val
 35          40          45
His Ser Ala Leu Phe Gln Gln Gly Leu Ile Gln Val Thr Leu Leu Cys
 50          55          60
Glu Gly Tyr Ser Ala Gly Glu Trp Lys Pro Gly Asp Gln Pro Gly Asp
 65          70          75          80
Tyr Cys Trp Ser Met Tyr Gly Gln Glu Met Thr Ser Gly Leu Asp Lys
 85          90          95
His Gly Gly Ser Glu Met Leu Gln Thr His Phe Tyr Thr Asp Asn Lys
 100         105         110
Lys Tyr Ala Val Asn Asp Val Ser Phe Ser Ile Pro Ala Ala Ser Glu
 115         120         125
Phe Ala Asp Leu Ser Asn Ile Ile Asn Lys Leu Leu Lys Asp Lys Asn
 130         135         140
Glu Phe His Lys His Met Glu Phe Tyr Phe Leu Ile Lys Gly Gln Phe
 145         150         155         160
Leu Arg Met Ser Leu Val Lys His Met Glu Leu Glu Asn Met Ser Ser
 165         170         175
Glu Val Val Val Glu Ile Glu Tyr Val Lys Tyr Thr Ala Pro Gln Pro
 180         185         190
Glu Gln Cys Met Phe His Asp Asp Trp Ile Leu Ser Val Lys Gly Ala
 195         200         205
Lys Glu Trp Ile Leu Thr Gly Ser Tyr Asp Lys Thr Ser Gln Ile Arg
 210         215         220
Ser Leu Glu Arg Lys Ser Ile Met Thr Ile Val Gly His Arg Asp Val
 225         230         235         240
Leu Lys Asp Val Ala Trp Ala Lys Lys Lys Asp Ser Leu Ser Cys Leu
 245         250         255
Phe Val Ser Ala Ser Met Asp Pro Thr Ile Leu Leu Trp Glu Trp Asn
 260         265         270
Arg Glu Lys Gln Ser Glu Ser Pro Thr Val Leu Gln Arg Ser Cys Trp
 275         280         285

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Lys Cys Arg Val Tyr Ser Cys
290 295

<210> 325

<211> 549

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)...(549)

<400> 325

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Met Glu Ala Glu Arg Leu Ser Gln Ser Ser Leu Ser Met Phe Leu Cys
1 5 10 15

ctg ctt ttt att cta tcc gtg ctg gca gct gat gag atg atg ccc acc 96
Leu Leu Phe Ile Leu Ser Val Leu Ala Ala Asp Glu Met Met Pro Thr
20 25 30

cag att gag gct act att acc ttc ttg ctt gtc acg ttg ctc att tac 144
Gln Ile Glu Ala Thr Ile Thr Phe Leu Leu Val Thr Leu Leu Ile Tyr
35 40 45

tcc tca ggg cca gct agg tgc ctg gag tct ccc ctg aaa gaa ctc aag 192
Ser Ser Gly Pro Ala Arg Cys Leu Glu Ser Pro Leu Lys Glu Leu Lys
50 55 60

att ttc ctt tat ttt cat gct cag cgc ggg ggt gcg gca gag gtc cct 240
Ile Phe Leu Tyr Phe His Ala Gln Arg Gly Gly Ala Ala Glu Val Pro
65 70 75 80

gct ctg tct cac tgg gac tat caa gtg tct ggt aca gaa aat aga gca 288
Ala Leu Ser His Trp Asp Tyr Gln Val Ser Gly Thr Glu Asn Arg Ala
85 90 95

act caa tgc agt tgc cgg ttt cag agc att ctt gaa ttg atc gtg aaa 336
Thr Gln Cys Ser Cys Arg Phe Gln Ser Ile Leu Glu Leu Ile Val Lys
100 105 110

cag ctt tcc agg tgc gat cgt ata aag gat cat tgg cag ctg tgc agc 384
Gln Leu Ser Arg Cys Asp Arg Ile Lys Asp His Trp Gln Leu Cys Ser

115	120	125	
ttg tca gct agc tgc aga aac cca ggt gtc atg ctg aca gct tca gtg			432
Leu Ser Ala Ser Cys Arg Asn Pro Gly Val Met Leu Thr Ala Ser Val			
130	135	140	
tta ata gcc ttt cag act tgg aga gcc agc atc cga cat aaa aat gat			480
Leu Ile Ala Phe Gln Thr Trp Arg Ala Ser Ile Arg His Lys Asn Asp			
145	150	155	160
agt ctt ata gag ttt gtt aat cag ctc tca aca ctg tgt aag aat aga			528
Ser Leu Ile Glu Phe Val Asn Gln Leu Ser Thr Leu Cys Lys Asn Arg			
165	170	175	
ccc ctg gat cgg ctt ctg tga			549
Pro Leu Asp Arg Leu Leu *			
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Leu Leu Phe Ile Leu Ser Val Leu Ala Ala Asp Glu Met Met Pro Thr			
20 25 30			
Gln Ile Glu Ala Thr Ile Thr Phe Leu Leu Val Thr Leu Leu Ile Tyr			
35 40 45			
Ser Ser Gly Pro Ala Arg Cys Leu Glu Ser Pro Leu Lys Glu Leu Lys			
50 55 60			
Ile Phe Leu Tyr Phe His Ala Gln Arg Gly Gly Ala Ala Glu Val Pro			
65 70 75 80			
Ala Leu Ser His Trp Asp Tyr Gln Val Ser Gly Thr Glu Asn Arg Ala			
85 90 95			
Thr Gln Cys Ser Cys Arg Phe Gln Ser Ile Leu Glu Leu Ile Val Lys			
100 105 110			
Gln Leu Ser Arg Cys Asp Arg Ile Lys Asp His Trp Gln Leu Cys Ser			
115 120 125			
Leu Ser Ala Ser Cys Arg Asn Pro Gly Val Met Leu Thr Ala Ser Val			
130 135 140			

Leu Ile Ala Phe Gln Thr Trp Arg Ala Ser Ile Arg His Lys Asn Asp
 145 150 155 160
 Ser Leu Ile Glu Phe Val Asn Gln Leu Ser Thr Leu Cys Lys Asn Arg
 165 170 175
 Pro Leu Asp Arg Leu Leu
 180

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<400> 327

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1 5 10 15	
ttg atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg	96
Leu Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu	
20 25 30	
gcc ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca	144
Ala Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro	
35 40 45	
gtg ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg	192
Val Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val	
50 55 60	
gga gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac	240
Gly Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp	
65 70 75 80	
gtg atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg	288
Val Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro	
85 90 95	
ctg ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg ccg gag cag ggc	336
Leu Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly	

	100	105	110	
act gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc				384
Thr Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly				
	115	120	125	
ccc gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg				432
Pro Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro				
	130	135	140	
cgc ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc				480
Arg Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly				
	145	150	155	160
gac atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc				528
Asp Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg				
	165	170	175	
gac ctg ccg cgt ctg ctg ccg gcg ctg gac gcg ccg cct ttc gca gag				576
Asp Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu				
	180	185	190	
gcc acc agc tgg ggc cgc ctt ggg gcg ccg cag cgc agg cag agc cgc				624
Ala Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg				
	195	200	205	
cta gag ctg tgc agc ccg ctt gaa cga gag gcc gcc cga ctt gca gac				672
Leu Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp				
	210	215	220	
cta ggt tga				681
Leu Gly *				
225				

<210> 328

<211> 226

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Ser	Ser	Trp	Gly	Gly	Gly	Val	Ser	Tyr	Arg	His	Leu	Gly	Leu
1				5				10					15		

Leu Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu
 20 25 30
 Ala Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro
 35 40 45
 Val Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val
 50 55 60
 Gly Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp
 65 70 75 80
 Val Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro
 85 90 95
 Leu Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly
 100 105 110
 Thr Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly
 115 120 125
 Pro Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro
 130 135 140
 Arg Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly
 145 150 155 160
 Asp Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg
 165 170 175
 Asp Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu
 180 185 190
 Ala Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg
 195 200 205
 Leu Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp
 210 215 220
 Leu Gly
 225

<210> 329

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide tag

<400> 329

Glu Tyr Met Pro Met Glu

1

5